

m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSDNDLEKERGITILAKNT
a151	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSDNDLEKERGITILAKNT
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL
a151	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
a151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRIGIGRILNGRIKPGQTVAVMN
a151	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRIGIGRILNGRIKPGQTVAVMN
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
a151	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLRQKELLTNVALRVEDTADADVFRVSGR
a151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLRQKELLTNVALRVEDTADADVFRVSGR
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
	GELHLTILLENMRREGYELAVGKPRVYRDIDGQKCEPYENLTVDVPPDNQGAVMEEELGR
a151	GELHLTILLENMRREGYELAVGKPRVYRDIDGQKCEPYENLTVDVPPDNQGAVMEEELGR
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
a151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK
a151	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
a151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq  
 1 ATGAAAaaca aaACCAaagt ctgGGacttc cCaccccgcc tttTCCactG  
 51 Gctgcttgcc gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCCGCG  
 101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```

151 CTCGTATTCC GCCTCTGCTG GGGCATTG GGCAGcgATA CCGCCCGTTT
201 CTCccgTtTC GTCCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCCGGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgccgc cgtcTCATTT CAagtccgca CGGGGCTTTT
351 Tgccgccaat gaaaacacct tcagcaCCAA cggctacctc aaccatttgg
401 tttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTC
451 AAGCTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

```

g152.pep
1 MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLLVFLF
51 LVFRLCWGIW GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAVH IAAVAAYRIF KKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

```

m152.seq
1 ATGAAAAACA AAACCAAAGT CTGGGACCTC CCCACCCGCC TTTTCCACTG
51 GCTGCTTGCC GCGTCCCTGC CCTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTCTG CCTTTTCCTG
151 CTCGTATTTC GCCTCTGCTG GGGCATTG GGCAGCGATA CCGCCCGTTT
201 TTCCCGTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGTAT CTGAAAAACG
251 GTATTCGCCA ACACATCCAG CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTCTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCACCT CAACTTTTTC
451 AAGCTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCAGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

```

m152.pep
1 MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLFVFLF
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLFVFLFLLVFRLCWGIW					
	:     :     :     :     :					
g152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLLVFLFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:     :     :     :     :					
g152	GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAVAAYRVFKKKNLILPMI					
	:     :     :     :     :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAVAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAILLLSX					
	:     :     :     :					
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAILLLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
1  ATGAAAAACA AAACCAAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151 CTCGTATTCC GCCTCTGCTG GGGCATTTGG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCCGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCCGA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTGCTTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCCGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTTGG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451 AAAGTCTGCG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFILFL
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*
  
```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVFLFLVFRLCWGIW					
	:     :     :     :     :					
a152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILFLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:     :     :     :     :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAVAAYRVFKKKNLILPMI					
	:     :     :     :     :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKKNLILPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAILLLSX					
	:     :     :     :					
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAILLLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```

g153.seq
1  atgggggtttg cttacAgtat gacgtatata gaggtCGGGA taccggaggc
51  ggcacccgtc ctttCgetGC CCGAGATgat gcgcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TGctgaCTTT cGGCGcgcCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTCCG TTCGGGCCCG CGTTTTATCT
351 GATGTTTCGG CTGTCGGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCAA ATCGGGCGGC TGACGGGGA TAATGCGGT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTccg
501 cgaAGTgcc gaatcccCCT GCGGGGTGTg cgGCGcggaA CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCTgac ggcggcggtT
601 GTTTTGATT TCCctgCcaa TATCctgccc attatGAttt cgtccAATCc
651 tgccgccaag GAGGcCAACA CCATCTTAG CGGCATCGCT TATATGTGGG
701 ACgaggcgga CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGGCGGCACG
801 GTTCGCTTTG CCGCGGGCGG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTTGT GATTATTATT
901 TTGATGTGTT CGTTCcaca TTATGCCGCG CGCGTCATTC CGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTIT GACGATGCTG TCCGCCTATT
1001 ATTTGACCCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```

g153.pep
1  MGFAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGNNAV
151 QTASBGKTC SRCLYFRDSA ESPCGVCGAE LYGGRPKSLs ISSAFLTAAY
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAARFAL PAGAKLSHL YRITEAVGRW SMIDIFVII
301 LMCSEHTYAA RVIPGSAAYV FCLVVILTML SAYYFDPRL WDKRASDGIA
351 FNETEKYD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```

m153.seq
1  ATGGCGTTTG CTACGGTAT GACGTATATC GAGGTGCGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CGGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTCCG TTCGGGCCCG CGTTTTATCT
351 GATGTTTCGG CTGTCAGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGA TAATGCGGT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCGTGCG CGTTTCTGAC GCGGCGGGT
601 ATTTTGATT TCCCTGCCAA TATCCTGCCG ATTATGATT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACgaggcgga CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCG
801 CTTGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTTGT GATTATTATT
901 TTGATGTGTT CGTTCcaca TTATGCCGCG CGCGTCATTC CGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```

m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VFFVSTLVAY

```



	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFDYGFGLAEVMFVLTFGAPVLFLLCLYV					
g153	MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFDYGFGLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
m153.pep	70	80	90	100	110	120
g153	YAALIRKQAYPALRLATRVMVRLRQAMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
	70	80	90	100	110	120
m153.pep	130	140	150	160	170	180
g153	LSVMLIRTSVSVQPQHVVYFQIGRLTGDNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
m153.pep	190	200	210	220	230	240
g153	LYRRRPKSLSSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGRDLI					
	190	200	210	220	230	240
m153.pep	250	260	270	280	290	300
g153	AAVIFSASILVFPVLKIAAMSVLIASARFALPTGAKKLSHLYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
m153.pep	310	320	330	340	350	359
g153	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLLDWKRASDGIAFNETEKHDX					
	310	320	330	340	350	

```

a153.seq
  1  ATGGCGTTTG  CTTACGGTAT  GACGTATATC  GAGGTCGGGA  TACCGGGTGC
51  GGCATCCGTC  CTTTCGCTGC  CCGAGATGAT  GCGCCTGATG  GTGTTTCAGG
101 ATTATGGTTT  TTTTGGCCGA  GTGATGTTTG  TGCTGACCTT  CGGCGCGCCG
151 GTTCTGTTTC  TGCTGCTGTG  CCTGTATGTC  TATGCCGCGC  TGATACGGAA
201 ACAGGCGTAT  CCTGCGCTGC  GTTTGGCAAC  GCGTGCTGATG  GTGCGCTTGA
251 GACAGGCGAT  GATGGTGGAT  GTGTTTTTTC  TTTTCACTTT  GGTGGCGTAT
301 ATCAAGCTCT  CGTCTGTGGC  AGAGGTTTCG  TTCGGATFCG  CGTTTTATCT
351 GATGTTTCGG  CTGTGCGGTA  TGCTGATTTC  GACTTCGGTA  TCGGTTCCCC
401 AGCATTTGGT  GTATTTTCAA  ATCGGGCGGC  TGACGGGGGA  TAATCGGGT
451 CAGACGGCAT  CGGAAGGTAA  AACCTGTTGC  AGCCCTGCCT  TGTATTTCCG
501 CGACAGTGCC  GAATCCCCCT  GCGGCGGTGT  CGGTGCGGAA  CTGTACCGCC
551 GACGGCCGAA  AAGTCTTAGT  ATTTTCGTCG  CGTTTCTGAC  GCGCGCGGTT
601 ATTTTGTATT  TCCCTGCCAA  TATCTGCCG  ATTATGATT  CGTCCAATCC
651 TGCCGCCACG  GAGGTCAATA  CCATCCTTAA  CGGCATCGCT  TATATGTGGG
701 ACGAGGGCGA  CAGGCTGATT  GCGGCGGGTA  TTTTCAGCG  GAGTATTTTG
751 TGCCCGGTAC  TGAAGATTGC  GGCAATGTCT  GTTTTGATTG  CGTCCGCCCC
801 CTTGCTTTG  CCAACGGGTG  CAAAGAAATT  GTCGCACCTC  TACCGCATCA

```

```

851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLCLLYV YAALIRKQAY PALRLATRV MRLQAMMVD VFFVSTLVAY
101 IKLSSVAEVR FGSFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL ISSAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHYYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGA
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSESPCGVCGAE					
a153	LSVMLIRTSVSVPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
a153	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGI AFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
51  CAAAAACAAC accttctCT CCGCCGCTCG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCCG TACCGCCATC GGGCAAAgcy GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcccG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCAACAGG CAGCGGCATC AAACCTCAAT CCGCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCT GTcgaATACA AAGGGCTgaa
951 TGTcggCATG GTTTCCGATG TCCCTTATTT TGACCGCAAT gacagCCTGC
1001 ACCcgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagcCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGCGGGCAAA ATGATTGAGT TGAACGATCA GCCTTCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTGG ATGACTTGCA GGTCAAATG GCGGATTGTC
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAAGTTT
1551 GGACAAAACC TTAAGagagc TtcaACCCGT CATTAACTC TTGAAGAAAA
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pap
1  MTDNSPPPNQ HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FVVKPRIDQ SGVTGLGLLL SGSYIAFTPG KSGEAKDVFQ
151 VQDIPPVTAI GQSGRLRLNI GKNDRIILNVN SPVLYENFMV GQIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLBNINAEQS KEHWKQFQT ALNKGILTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVAELN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQTQ KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSKDIPIK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

ml54.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTTCATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCCGC
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCTG
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCCG TACCGCCATC GGGCAAGCGG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCAACAGG CAGCGGCATC AAACCTCAAT CCGCCCTCT GCCTGCCCTG
751 CTGTGCGGCG CGATTTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCCGACG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAGC AAAGAACATT GGAACAACA
1101 ATTTACAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCGCA

```

```
1201 TCACCTAAGC TGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACT TTAAGAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTT AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```
m154.pep
1  MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTPG KSDEAKDVFG
151 VQDIPPVTAI QSGRLRLNLI GKNDRIILNVN SPVLYENFMV QVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIEIPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTYV AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAEIN
451 GSLAELKSTL KSANAALSSI DKLVGKPTQ NIPNELNQL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*
```

m154 / g154 97.8% identity in 553 aa overlap

```
10 20 30 40 50 60
m154.pep MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE
g154 MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE
10 20 30 40 50 60
70 80 90 100 110 120
m154.pep GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ
g154 GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ
70 80 90 100 110 120
130 140 150 160 170 180
m154.pep SGVTGLGLTLLSGSYIAFTPGKSDEAKDVFGVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN
g154 SGVTGLGLTLLSGSYIAFTPGKSDEAKDVFGVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN
130 140 150 160 170 180
190 200 210 220 230 240
m154.pep SPVLYENFMVQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI
g154 SPVLYENFMVQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI
190 200 210 220 230 240
250 260 270 280 290 300
m154.pep KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
g154 KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
250 260 270 280 290 300
310 320 330 340 350 360
m154.pep SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIEIPS RLEINADEQS
g154 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIEIPS RLEINADEQS
310 320 330 340 350 360
370 380 390 400 410 420
m154.pep KEHWKQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG
g154 KEHWKQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATRG
```

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDIQVKLADLLDKFDKLPDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPKQTQ					
	:     :     :     :     :					
g154	GGLDDIQVKLADLLDKFNNLPDKTVAELNGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNENQLTKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	:     :     :     :     :					
g154	NIPNENQLTKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
	:					
g154	NNSSKDPKPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154 . seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAA
251 TCGCGGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCTT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AACTCAATT CCGCCCTCTT GCCTGCCCTG
751 CTGTGGGCGC CGATTTCATT TGATTCGCCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTC CGACAGCCCG AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTCGCCTT GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGGATG TTCCTTATT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAT TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGCACCACA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GGCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGCG
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTCG CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCCACTC AATCTGCCA ATGCCGCCCT
1401 AAGTCCATC GACAACTGG TCGGCAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAATACGCG TGCAAAGTTT
1551 GGACAAAACC TTAAGAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCAACGCG GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ

```

151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV QQVESAHFDP  
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL  
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ  
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS  
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA  
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN  
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT LKELRTTQGV  
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK  
551 GSR\*

m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNHQAQARVRKNN	TFLSAVWL	VPLIALI	AGGWLWV	KEIRNRGP	VVTLMLMSAE
a154	MTDNSPPPNHQAQARVRKNN	TFLSAVWL	VPLIALI	AGGWLWV	KEIRNRGP	VVTLMLMSAE
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVIK	VSIDVGRV	TRIKLRDD	QKGVEVTA	QLNADVSG	LIRSDTQFWVVKPRIDQ
a154	GIEVNNTVIK	VSIDVGRV	TRIKLRDD	QKGVEVTA	QLNADVSG	LIRSDTQFWVVKPRIDQ
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTL	LSGSYIA	FTPGKSDE	AKDVQVQ	QDIPPVTA	IGQSGRLRLNLIGKNDRIILNVN
a154	SGVTGLGTL	LSGSYIA	FTPGKSDE	AKDVQVQ	QDIPPVTA	IGQSGRLRLNLIGKNDRIILNVN
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFM	VGVQVES	AHFDPSD	QSVHYTIF	IQSPNDK	LIHSASRFWLESGINIETTSGSI
a154	SPVLYENFM	VGVQVES	AHFDPSD	QSVHYTIF	IQSPNDK	LIHSASRFWLESGINIETTSGSI
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLP	PALLSG	AISSPK	TKNKNSK	NKSVKSE	DSFTLYDSRSEVANLPDDRSLYYTAFFKQ
a154	KLNSAPLP	PALLSG	AISSPK	TKNKNSK	NKSVKSE	DSFTLYDSRSEVANLPDDRSLYYTAFFKQ
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVG	SPVEYK	GLNVGV	VSDVPY	FDRNDSL	HLFENGWIPVRIRIEPSRLEINADEQS
a154	SVRGLTVG	SPVEYK	GLNVGV	VSDVPY	FDRNDSL	HLFENGWIPVRIRIEPSRLEINADEQS
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQQF	QTALNK	GLTATIS	SSNNLL	TGSKMIE	LNDQPSASPKLRPHTVYAGDTVIATQG
a154	KEHWKQQF	QTALNK	GLTATIS	SSNNLL	TGSKMIE	LNDQPSASPKLRPHTVYAGDTVIATQG
	370	380	390	400	410	420
m154.pep	430	440	450	460	470	480
	GGLDDLQV	KLADLL	DKFDKL	PLDKTVA	ELNGSLA	EKSTLKSANAALSSIDKLVGKPTQ
a154	GGLDDLQV	KLADLL	DKFDKL	PLDKTVA	ELNGSLA	EKSTLKSANAALSSIDKLVGKPTQ
	430	440	450	460	470	480
m154.pep	490	500	510	520	530	540
	NIPNELNQ	TLKELRT	TTLQGV	SPQSPIY	GDVQNTL	QSLDKTLKDVQPVINTLKEKPNALIF
a154	NIPNELNQ	TLKELRT	TTLQGV	SPQSPIY	GDVQNTL	QSLDKTLKDVQPVINTLKEKPNALIF
	490	500	510	520	530	540

```

                    550
m154.pep  NSSSKDPIPKGSRX
          |||||
a154      NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1  atGAAaatcg GtatcCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gccACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGCGGTTT GGGCCTGCCC
201 TTTAATTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGCAGCG CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCCCCG ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCGGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcttGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCTCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCCGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGCGT GAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaaATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CGGccgaTTc aggtTTCgc cgggcccGAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tgmtCCctg
1201 tggAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcacccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGCTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGatgtcggt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAAATCG GTCAGGGcaa cggcttcgtT TCgctGCTGT
1451 CGTTTGTTC CATCTGATT GCCGCGATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTI SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTQGITAA GKVPQAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFLOES GSGDGYAKV MSDEFIAEM KLFQEQAKEV
251 DIIITTAAP GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTGNGVKII GYTDMANRLA GQSSQLYATN LVNLTLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIQGNGFV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMEK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1  ATGAAAATCG GTATCCCACG CGAGTCATTA TCCGCGGAAA CCCGCGTCGG
51  CTGTACGCCG GCCACCGTCG CCCTGCTGGG CAAACTGGG TTTGAAACCG
101 TTGTCGAAG CGGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAAGT CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

```

301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCCG ATTTGCGCGG CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CCGGTACCGC GCGTAATTG AAGCCGCCAA CGCCTTCGCG
451 CGTTTCTTCA CCGGTCAAAT TACCGCGGCC GGCAAAGTGC CGCCCGCGCA
501 GGTGTTTGGTG ATTGGTGAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGCAGCGGC GGCAGTGGC AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAATC ATCGGTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCG
1201 CTGTGAAAAA AACTCGCGCC CGCCGTCTAT GCCCGCTCT TGGTACTGTG
1251 GGTGCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGGCA TCAACATCTT CGGCGGCTTT
501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51 QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTI V SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAAP GKPAKPLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVGI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QOTPSEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVGVA VAPAAFLNHF IVFVLACVIG YVYVWNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQGNF VLLSFLVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155           MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep      AAVWVCPLIYKVNAPSEQELPLLNEGQTI V SFLWPRQNEALVEALRAKKVNALAMDMPVR
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g155           AAVWACPLIYKVNAPSEGE LPLLKEGQTI V SFLWPRQNEALVEALRAKKVNALAMDMPVR
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep      ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155           ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGQITAAGKVPPAQVLVIGAGVAGLAA

```



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	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
m155.pep	370	380	390	400	410	420
	VTHDGEITFPFPPIQVSAQPQQTPESEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
g155	VTRDGEITFPFPPIQVSAQPQQTPESEKAAAPAKPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
	360	370	380	390	400	410
m155.pep	430	440	450	460	470	480
	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIIVVGALLQIQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIQGNGF					
	420	430	440	450	460	470
m155.pep	490	500	510			
	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAATCG GTATCCACG TGAGTCATTA TCCGGCGAAA CCCCGCTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGNTTG TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGGCGAGCG GCGACGGCTA CGCAAAGTG ATGAGCGACG
701 AATTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGACGGGC GGCAACTGCG AACTCACCAA ACAGGCGGAA
901 TTGTTTCGTAA CCGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCAAGC CCGAACCGAA ACCCGTTCCC

```

```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGCGCGCG GTGCGACCCG CAGCATTCTT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIY SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAAG
151 RXFTGQITAA GKVPAPQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAaip GKPAKXXXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LEVFTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVVGA VAPAAFLNHF IVFVLACVIG YVVVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQGNF VSLLSFVAIL IASINIFGGF
501 FVTRRMLNMF RKG*

m155/a155 95.3% identity in 513 aa overlap

      10      20      30      40      50      60
m155.pep  MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
a155      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK
      10      20      30      40      50      60

      70      80      90      100     110     120
m155.pep  AAVWVCPLIYKVNAPSEQELPLLNEGQTIYSFLWPRQNEALVEALRAKKVNALAMDMPVR
a155      AAVWAYPLIYKVNAPSEDELPLLKEGQTIYSFLWPRQNEALVEALRAKKVNALAMDMPVR
      70      80      90      100     110     120

      130     140     150     160     170     180
m155.pep  ISRAQALDALSSMANISGYRAVIEAANAAGFRFTGQITAAGKVPPAQVLVIGAGVAGLAA
a155      ISRAQALDXLSXMANISGYRAVIEAANAAGFRXFTGQITAAGKVPPAQVLVIGAGVAGLAA
      130     140     150     160     170     180

      190     200     210     220     230     240
m155.pep  IGTANSLGAVVRAFDTRLXVAEQIESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM
a155      IGTANSLGAVVRFDTLXVAEQLESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM
      190     200     210     220     230     240

      250     260     270     280     290     300
m155.pep  KLFAEQAKEVDIIITTAaipGKPAKPLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE
a155      KLFAEQAKEVDIIITTAaipGKPAKXXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE
      250     260     270     280     290     300

      310     320     330     340     350     360
m155.pep  LSVTNGGVKIIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
a155      LEVFTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
      310     320     330     340     350     360

      370     380     390     400     410     420
m155.pep  VTHDGEITFPPIQVSAQPQQTPEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVVGA
a155      VTRDGEITFPPIQVSAQPQQTPEKAAPAAKPEPKPVPLWKKLAPAXIAAVLVLVVGA
      370     380     390     400     410     420

```

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```

          430      440      450      460      470      480
m155.pep  VAPAAFLNHFIVFVLACVIGYVVVWNVSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF
          |||||||
a155      VAPAAFLNHFIVFVLACVIGYVVVWNVSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF
          430      440      450      460      470      480

          490      500      510
m155.pep  VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX
          |||||||
a155      VSLLSFVAILIASINIFGGFFVTRRMLNMFKKGX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTCTCG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCCGCCGC
201 CGTTTGTACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATGTGTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGCGCG GCGGATTGCG
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LERLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGGTTTCTTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCCGCCGC
201 CGTTTGTACG GCACACGCAA CCGGCAATGC GCGGCAATCG ACCATCAACA
251 CGCTTGCCGT CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTGCG
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAAQS TINTLACLFI LERLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

```

          10      20      30      40      50      60
m156.pep  MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
          |||||||
g156      MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
          10      20      30      40      50      60

          70      80      90      100     110     120
m156.pep  FAPFAAAVLTAHATGNAAQSTINTLACLFILERLAFIWCYIADKAAMRSLMWAGGFACTV
          |||||||
g156      FAPFAAAVLTAHATGNAAQSTINTLACLFILERLAFIWCYIADKAAMRSLMWAGGFACTV
          70      80      90      100     110     120

```

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
            |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351 CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51  HAAQQNGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LRLAFIWCY
101 IADKAALRSL MWVGGEVCTV GLFVAA*

m156/a156  90.6% identity in 127 aa overlap

              10      20      30      40      50      60
m156.pep    MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAARAHAQQNGFEA
            |||||
a156        MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAQQNGFEA
              10      20      30      40      50      60

              70      80      90      100      110      120
m156.pep    FAPFAAAVLTAHATGNAAQSTINTLACLFI LRLAFIWCYIADKAAMRSLMWAGGFACTV
            |||||
a156        FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGEVCTV
              70      80      90      100      110      120

m156.pep    GLFVAAAX
            |||||
a156        GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgcctgcgc cgcgaattgC gCgGgcggcg
51  ttcgcAAATg GGgcgagacg tGCGggCGGC GGCGgCgatA Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCgGCGCA AAactctatc tgccttATAT CGAACCgCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401 GCTACCGTTT GGGGCAGGCA GGCGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTTCAGGC GAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
51  PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMERERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
1  ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCAATTGC GCGGGCGGCG
51  TTCGCAAATG GGGCGGGACG TGGCGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACC CGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTGCGA AAAAGCGTGT
351 GCATGATTTG AACCTCCTGC TTGTGCCAGT GGTCGGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAAATV KINHLLKRYI KKGRKIGVYW
51  PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
101 GRAKLHVPQF AGRKKRVHDL NLLVPPVVG DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMGRDVRAAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKIRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRMWFTYPERGMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	NLLVPPVGM DRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGI DREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
1  ATGAGGAACG AGGAAAAACA CGCCTTGC GCAGAGTTGC GCCGCGCCCG
51  CGCGCAGATG GGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAAAC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
1  MRNEEKHALR RELRRARAQM GHQRLAAGQ TINRLKRYI KRGRKIGVYW
51  PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYP ESMERERIR
101 GRAKLNVQF AGRKIRVHGL SVLLVPLVGI DREGYRLQA GGYDATLAA
151 MKYRLQAKTV GVGACQFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

```

              10      20      30      40      50      60
m157.pep    MRNEEKRALRRELRRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG
              |||||:||||| |:|::: | |  ||:|||||:|||||:|||||
a157         MRNEEKHALRRELRRARAQMGGHQRRLAAGQTINRLKRYIKRGRKIGVYWPMGKELRLDG
              10      20      30      40      50      60

              70      80      90      100     110     120
m157.pep    FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKGRAKLHVLPQFAGRKKRVHDL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a157         FVRAAQKRGAKLYLPYIEPRSRMWFTYPESGMRERIRGRAKLNVLPQFAGRKIRVHGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m157.pep    NLLVVPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
              ::|||:|:| | |||||:|||||:|||||:|||||:||||| | |
a157         SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL
              130     140     150     160     170     180

              190
m157.pep    LDGFVSEAGILCFX
              |||||:|||||
a157         LDGFVSEAGILCFX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
1  ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51  CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATCTTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAACCTGCTc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGCT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATCAACGA
351 ACGCTATCCG CATATCcgac TTTGCTCGT TTCTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAagtt
701 gCGGTATTGC TTGCTTATCA GATTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG  
 851 TATTTTTGGA TTTTITAGTG AAGGAAGTGG GAAAAATAT GAATAGAACG  
 901 AATACCAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep  
 1 MKTNSEELTV FVQVVEGSGF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTRQLNLT EEGAQYFRR QRIQEMAAA ETEMLAVHEV PQGVLRVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE  
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR  
 301 NTK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq  
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG  
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG  
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC  
 151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT  
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA  
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATCCGCG  
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATCAACGA  
 351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTCCGAA GGCTATATCA  
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCCCG AGAATTGGAC  
 451 GATTCCGGGC TCGGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT  
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG  
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT  
 601 ACATGGGCGG TTTTAGATGC GCAGGGAAT CCCTATAAGA TTTACCCGCA  
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT  
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGTGA  
 751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC  
 801 CTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG  
 851 TATTTTTGGA TTTTITAGTG GAGGAAGTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep  
 1 MKTNSEELTV FVQVVEGSGF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTRQLSLT EEGAQYFRR QRIQEMAAA ETEMLAVHEI PQGVLSVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE  
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNLCCG\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTRQLSLT					
g158	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTRQLNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRQRIQEMAAAEETEMLAHVHEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYP					
g158	EEGAQYFRRQRIQEMAAAEETEMLAHVHEVPQGVLRVDSAMPVHLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSGCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTHPFNAVYSDKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTCAAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCCCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTGTGA	TTTTTTAGTG	GAGGAACG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRR	QRILQEMAAA	ETEMLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQ	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRQRILQEMAAEETEMLAVHEIPQGVLSVDSAMPMVLHLLAPLAAKFNERYP					
a158	EEGAQYFRRQRILQEMAAEETEMLAVHEIPQGVLRVDSAMPMVLHLLAPLAAKFNERYP					
	70	80	90	100	110	120



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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCcCaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCCGCGTCC  GGTGCGCACG  GCGGATATTG  TATTTTCCCG
201 GCGCGGCTTG  GGTCATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CACACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAAC  CGTTTTCTG  AACATTGCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGCTCAAC  GCATTACCGT  CCGTCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTGGGACA  TTGATCCAA
601 AAGGTGATAG  ACAAAACCGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGCGCGCC  TTTGTGAACC  ATATCCGCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCCGGATTTC  GTTTGGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTTCG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVDN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GAAAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGGCGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCC  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTC

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501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

-- This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL
  51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
 101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
 151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
 201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
 251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
 301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

	10	20	30	40	50	60
m160.pep	MDILDKLVDF	AQLTGSVDVQ	CLLGGQSVR	HETLQREGLV	HIVTSGSGYL	CIDGETSPRP
g160	MDILDKLVDLA	QLTGSADVQ	CLLGGQW---	HETLQREGLV	HIVTAGSGYL	CIDGETSPRP
	10	20	30	40	50	
	70	80	90	100	110	120
m160.pep	VSTGDIVFFP	RGLGHVLSHD	GKCGESLQPD	MRQHGAFTVK	QCGNGQDMSL	FCARFRYDTH
g160	VGTGDIVFFP	RGLGHVLSHD	GKYGESLQPD	IRQNGTFMV	KQCGNGLDMS	LFCARFRYDTH
	60	70	80	90	100	110
	130	140	150	160	170	180
m160.pep	ADLMNGLPET	VFLNIAHPSL	QYVVSMLQLE	SKKPLTGTVS	MVNALSSVLL	VLILRAYLEQ
g160	ADLMNGLPET	VFLNIAHPSL	QYVVSMLQLE	SEKPLTGTVS	VVNALPSVLL	VLILRAYLEQ
	120	130	140	150	160	170
	190	200	210	220	230	240
m160.pep	DKDVELSGVL	KGWQDKRLGH	LIQKVIDKPE	DEWNVDMVA	AANMSRAQLM	RRFKSRVGLS
g160	DKDVELSGVL	KGWQDKRLGH	LIQKVIDKPE	DEWNVDMVA	AANMSRAQLM	RRFKSQVGLS
	180	190	200	210	220	230
	250	260	270	280	290	300
m160.pep	PHAFVNHIRL	QKGALLLKNP	PDSVLSVALS	VGFQSETHFG	KAFKRQYHVS	PGQYRKEGGQ
g160	PHAFVNHIRL	QKGALLLKNP	PDSVLEVALS	VGFQSETHFG	KAFKRQYHVS	PGQYRKEGGQ
	240	250	260	270	280	290
m160.pep	KX					
g160	KX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
  1 ATGGACATTC TGGACAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
 51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```

101 TGCAACGCGA AGGATTGGTA CACATTGTGA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAATATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCAGCA ACGGACAGGA TATGAGCCTG TTTGCGCCCC GTTTCGCTA
351 CGACACCCAC GCCGATTTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCC TCCGAGTTTA CAGTATGTGG TTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTGTCG AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTCGGT
801 CGCACTGTGC GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMAA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

m160.pep      10      20      30      40      50      60
MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
|||||
a160          10      20      30      40      50      60
MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP

m160.pep      70      80      90     100     110     120
VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
|||||
a160          70      80      90     100     110     120
VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH

m160.pep     130     140     150     160     170     180
ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGT VSMVNALSSVLLVLILRAYLEQ
|||||
a160         130     140     150     160     170     180
ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGT VSMVNALSSVLLVLILRAYLEQ

m160.pep     190     200     210     220     230     240
DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMAA AANMSRAQLM RRFKSRVGLS
|||||
a160         190     200     210     220     230     240
DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMAA AANMSRAQLM RRFKSRVGLS

m160.pep     250     260     270     280     290     300
PHAFVNHIRL QKGALLLKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
|||||
a160         250     260     270     280     290     300
PHAFVNHIRL QKGALLLKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ

m160.pep      KX
               ||
a160          KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGCGCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGCTGCTG CTCCTTGATT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTACAGAA
451 CCGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACC CGC TGCGCGTTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGCGCA TGTCTGCGgt ttgggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCgtcCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGCGCA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTCTCTg ggcgaaagac ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMFLS
51  TVTLGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGCGCTGC TTTACCATT A TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCCGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGCTGCTG CTCCTTGATT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTACAGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACC CGC TGCGCGTTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCTGCGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGCGCA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLS
51  TVALGAAAVL RRDXTFTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVLL LNPSFRSGQE

```

Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50	60
m161.pep		MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLFSTVALGAAAVL      :     :     :     :     :					
q161		MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMLFSTVTLGAAAVL 10 20 30 40 50 60					
		70	80	90	100	110	120
m161.pep		RRDXFRTPHWKHNLRSMVG TGAMLLLFYAVTHLPLATGVTL SYTSSIFLAVFSFLIKE    :     :     :     :     :					
q161		RRDTFRTPHWKHNLRSMVG TGAMLLLFYAVTHLPLTTGVTL SYTSSIFLAVFSFLIKE 70 80 90 100 110 120					
		130	140	150	160	170	180
m161.pep		RISVYTQAVLLLG FAGVVLLNPSFRSQETAALAGLAGGAMSGWAYLKVRELSLAGEPG      :     :     :     :     :					
q161		RISVYTQAVLLLG FAGVVLLNPSFRSQEPAALAGLAGGAMSGWAYLKVRELSLAGEPG 130 140 150 160 170 180					
		190	200	210	220	230	240
m161.pep		WRVVFYLSVTGVAMSSVWATLTGWHTLSFP SAVA YLSCIGVSALIAQLSMTRAYKVGDKFT      :     :     :     :     :					
q161		WRVVFYLSATGVAMSSVWATLTGWHTLSFP SAVA YLSCIGVSALIAQLSMTRAYKVGDKFT 190 200 210 220 230 240					
		250	260	270	280	290	300
m161.pep		VASLSYMTVVFSA LSAAFFLGEELFWQEILGMCI IILSGILSSIRPTAFKQR LQSLFRQR      :     :     :     :     :					
q161		VASLSYMTVVFSA LSAAFFLGEELFWQEILGMCI IILSGILSSIRPIAFKQR LQALFRQR 250 260 270 280 290 300					
m161.pep	X						
q161	X						

```

a161.seq
  1  ATGGATACCG CAAAAAAGA CATTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGGCGGCTCG TTTACCATTA TGAACGTATT GATTAAGAAG GCATCGGGACA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTC A
151 ACCGTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCCGCAC
201 GCCCATTGG AAAAACCACT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCCTTTGGC CACCCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTT GCGGTATTTT CCTTCCGTGAT
351 TTTGAAAGAA CGGATTTTCCG TTTACACGCA GCGCGTGCCT GTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCGCAG CGGTCAAGAA
451 ACGGCGGCAC TCGCCGGGCT GGGGGGCGGC GCCATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CCGCAACTGT TCTTGGCGGG CGAACCCTGG TGGGCGGCTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCATCGGT TTTGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTACAG GTTGCCCTCG TTTCTATAT GACCCCTGTT
751 TTTTCCGCTC TGTCTGCCG ATTTTTCCTG GCCGAAGAGC TTTTCTGGCA
801 GGAATACTC GGTATGTGCA TCATCATCTC CAGCGGTATT TTGAGCAGCA

```

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA  
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep  
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVEWRMLFS  
51 TVALGAAAVL RRDTRTPHW KNHLNRSMSGV TGAMLLLFYA VTHLPLATGV  
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE  
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVMSSVWAT  
201 LTGWHTLSFP SAVYLSICGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV  
251 FSALSAAFFL AEELFWOEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR  
301 \*

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSMSGVTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSMSGVTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
a161	WRVVFYLSVTGVMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWOEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEEELFWOEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
	I					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq  
1 ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTTGG TGGTATTGGT  
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAGAAG  
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTtTt  
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGTtTGGGAA ACATcagGCT  
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA  
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA  
301 GAGCCGTGA TGCATTATT TTCGACATT ACGGTCGGCG CGCCGGAACA  
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCAGC  
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTITTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCCT TTTTGCTGCT GTTTTTTGTG TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGgC
951 gcCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCGGGGTT TTGCTCATCC CCGGCTGTG CCGCGTTTTC
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACTTCT GCCGACTCCG GGATTTATGT
1251 CTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCTT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTACGCTG TGGAAAGGCT
1451 TGAGTGCGBA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGBA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTGCTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

```

g163.pep
1  MVILTTLFFV CVLVVLVLTV PDQVMWLDL AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSEINL
251 GLAFLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFEWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLEKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITSRDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLOS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

```

m163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CCGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACG
401 CTTGGTCGGT GTACGCTACG ATTGCATTGG CTTTGGCTTA TTTGCGTTT
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTITTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TCTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTAACT ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGCGGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGCGG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAAGTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTLFFV CVLVVLVLT VPDQVQMWLDRAKEVIFTEFSWFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLEFAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKPLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPEV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITSRLKGLSA PRWQAVMWG LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQDEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
g163	MVILTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
	10	20	30	40	50	60
m163.pep	SLGNIRLGRDEDVPEFGFLSWLAMLEFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDEDVPEFGFLSWLAMLEFAAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180



m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSEINLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSEKTYAYEREHKP
g163	GVKVLSEINLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSEKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKHTASPAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGACAGTT TTGATTATCG CCGCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCGT TTTTGCTGCT GTTTTGTGTT TTGGCGCGCG GTCCACTGT
801 TTACCTGTTG TCGGCATTGC GCGACAACAT AGGGAACATC CTCGGAAATC
851 TGGTGCCTCT CAGTTTAAAA ACTTATGCGT ACGAACGGGA ACACAGCCG
901 TGGTTTGAAT CTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGG
951 GCCGTTTGTG GGTTTGTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 CGGAGTTTGT CTTGGGGGTT TTGCTCATCC CCGGCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGAAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CTGCGAGTCT ATGACCCTGA TGTTCCTCT
1401 CCGGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGAT
1451 TGAGTGCAGG TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGACGA TAATGAGCCA
1551 GACGACAGGAG CAGGATATTT TAAATTCTCT CAAACATACC GCATCGCCG
1601 CTATGCACGA GTTACAAACG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CCGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAACGT
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWCWSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WETVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFEVTS ADGGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCPSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTPYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

              10      20      30      40      50      60
m163.pep      MVILTTLFFV CVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
              |||||
a163           MVILTTLFFV CVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS
              10      20      30      40      50      60
              70      80      90     100     110     120
m163.pep      SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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```
|||||
a163 SLGNIRLGRDEVDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m163.pep QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
      |||||
a163 QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
      130     140     150     160     170     180

      190     200     210     220     230     240
m163.pep MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
      |||||
a163 MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
      190     200     210     220     230     240

      250     260     270     280     290     300
m163.pep GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
      |||||
a163 GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
      250     260     270     280     290     300

      310     320     330     340     350     360
m163.pep WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVGVLLIPGLFGLVWFTVFGNTAI
      |||||
a163 WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVGVLLIPGLFGLVWFTVFGNTAI
      310     320     330     340     350     360

      370     380     390     400     410     420
m163.pep WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
      |||||
a163 WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
      370     380     390     400     410     420

      430     440     450     460     470     480
m163.pep ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
      |||||
a163 ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
      430     440     450     460     470     480

      490     500     510     520     530     540
m163.pep WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPAHMLQR
      |||||
a163 WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKHTASPAHMLQR
      490     500     510     520     530     540

      550     560     570     580     590     600
m163.pep ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
      |||||
a163 ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
      550     560     570     580     590     600

      610     620     630     640     650     660
m163.pep HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
      |||||
a163 HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
      610     620     630     640     650     660

m163.pep X
      |
a163 X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1 ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51 CAAGGCGCGC TTCCTGTTCC CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAA TCATTGGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCGC ACTTGGGCGC CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCcC ttttccaacG TTTTGAAAAA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAAGAT GTTCAACCGC
601 ATCCGCTGTG TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGGCGA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAACACG GGCATTTTCG TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCAT GCGGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGCG
1151 GCGAGGACGA aatccgccc caccTGCCTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1 ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51 RPAGETAEGD AFFENVRRFP EKPDLRQPR INDLAHIIT SGTGHPKGA
101 LISYANLEAF LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWENR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLL GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKKD LIISKGQNVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1 ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51 CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251 TACCGATGAA CACATTTTGT AAAAAACGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTGGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTC CAACGTTTTC
751 AAACAGACAC TGCTCAAACG CGGACCGGTG TTTTGGGCGG TACCCGCGAT
801 TTACACCGCG ATAGCAAGG CGAAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATTTC CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA

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466

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCTGCG CCGGTTTGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGGCTA CCTCAATATG CTGCGCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTGAT
1251 TATTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGD AFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQTLKRATV FLGVP AIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGLIVRG GSVMRGYLNM PAATDETIVN GWLKTGFVFT
401 IDEGDFIFIV DRKKDLIISK GQNVYPREIE EEIYKLD AVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGVVLRV LK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:  
 Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

m164.pep	60	70	80	90	100	110
	GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK					
g164	MNTFLKNSEYAYILNDCKARFLFASAGLSK					
	10	20	30			
m164.pep	120	130	140	150	160	170
	ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT					
g164	ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT					
	40	50	60	70	80	90
m164.pep	180	190	200	210	220	230
	SGTTGHPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMAC					
g164	SGTTGHPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMAC					
	100	110	120	130	140	150
m164.pep	240	250	260	270	280	290
	SIILVKSVPFNSNVLKQTLKRATVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP					
g164	SIILVKSVPFNSNVLKQALLKRATVFLGVP AIYTAMSKAKIPWYFRWFNRIRLFISGGAP					
	160	170	180	190	200	210
m164.pep	300	310	320	330	340	350
	LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVG IPLPGLEAKAVDEEL					
g164	LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVG IPLPGLEAKAVDEEL					
	220	230	240	250	260	270
	360	370	380	390	400	410

467

```

m164.pep  VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      LIISKQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTG AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCTCG GCCGCGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAA CGCCGTCGA AAAATCATT TGGACGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCGCT TCCCCGAAA ACCCGACTTG GGCCGCCAAC CCGGATAAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCTTTTC CAACGTTTG
751 AAACAGGCAC TGCTCAAACG CGGACCGTG TTTTGGGCG TGCCCGGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCGTGTATAT AGCGGCGGAG CACCTTTGCG GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCGCG GCCAAATTGC TGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGCTA CCTCAATATG CCGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAAT
1451 TCAAAATCCC CAAACAAATC CACTTTAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTT ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKN NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPALYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLIISK QNVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRTV LANFKIPKQI HFKDGLPRNA

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468

501 TGKVLKRVLK EQFDGNK\*

m164/a164 98.3% identity in 517 aa overlap

	10	20	30	40	50	60
m164.pep	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIQVKGFDTV					
a164	MNRTYANFYEMLTAAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIQVKGFDTV					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
a164	LAVSNSTEFITAYFAISAIGAVVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
a164	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
a164	HPKGALISYANLFANLNGIERIFKISKDRDFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
a164	KSVFPFSNVLKQTLKQATVFLGVPPIYATMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
a164	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHRTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq  
 1 ATGGCTGAAG CGACAGACGT TGTCTGGTG GCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGGca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCG cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTAAAA
401 CGCAGAAACT TTTTGAATAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaa ACCAACCCGT
501 CGCCGCCAAC TATTCGCCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGCGCGG GCGGCGCGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CctGTGGGc gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCRYLQKRYD VFRTQKLFEN MEFSTDNRKI
151 SDWAPLMRG RDENQPVAA N YSAEGTDVDF GRLTRQMKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLQK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYFMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTTGTTCT ATCTTCAAAA ACGTTATGAC GCGTTAAAA
401 CCCAAAAACT TTTTGAATAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGCGCGG GCGGCGCGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCRYLQKRYD VFRTQKLFEN MEFSTDNRKI
151 SDWAPLMRG RDENQPVAA N YSAEGTDVDF GRLTRQMKY LQKGKVKTEF

```



201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK  
 251 SGIPEGKGYG GFPVSGLFRR NSNPETAEOH NAKVYQASV GAPPMSPVPHL  
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA  
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLEDVA	LESSNAWNNAGTGH	SALC		
g165	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLEDVA	LESSNAWNNAGTGH	SALC		
	10	20	30	40	50	60
m165.pep	ELNYAPLGANGIIDPARALNIAEQ	FHVSQFWATLVAEGKLEDNSFI	NAVPHMSLVMNED			
g165	ELNYAPLGADGVINPARALNIAEQ	FHVSQFWATLVAEGKLEDNSFI	NAVPHMSLVMNED			
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQ	FHVSQFWATLVAEGKLEDNSFI	NAVPHMSLVMNED			
g165	ELNYAPLGADGVINPARALNIAEQ	FHVSQFWATLVAEGKLEDNSFI	NAVPHMSLVMNED			
	70	80	90	100	110	120
m165.pep	HCSYLQKRYDAFKTQKLFENMEF	STDNRKISDWAPLMRGRDENQP	VAAANYSAEGTDVDF			
g165	HCRYLQKRYDVFKTQKLFENMEF	STDNRKISDWAPLIMRGRDENQP	VAAANYSAEGTDVDF			
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEF	STDNRKISDWAPLMRGRDENQP	VAAANYSAEGTDVDF			
g165	HCRYLQKRYDVFKTQKLFENMEF	STDNRKISDWAPLIMRGRDENQP	VAAANYSAEGTDVDF			
	130	140	150	160	170	180
m165.pep	GRLTRQMVKYLQGGKGVKTEFNR	HVEDIKRESDGAWVLKTADTRN	PDGQLTLRTRFLFLGA			
g165	GRLTRQMVKYLQGGKGVKTEFNR	HVEDIKRESDGAWVLKTADTRN	PDWQLTLRTRFLFLGA			
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLQGGKGVKTEFNR	HVEDIKRESDGAWVLKTADTRN	PDGQLTLRTRFLFLGA			
g165	GRLTRQMVKYLQGGKGVKTEFNR	HVEDIKRESDGAWVLKTADTRN	PDWQLTLRTRFLFLGA			
	190	200	210	220	230	240
m165.pep	GGGALTLLQKSGIPEGKGYGGFP	VSGLFFRNSNPETAEOHNAKVY	QASVGA	PMPSPVPHL		
g165	GGGALTLLQKSGIPEGKGYGGLP	VSGLFFRNSNPETAEOHNAKVY	QASVGA	PMPSPVPHL		
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFP	VSGLFFRNSNPETAEOHNAKVY	QASVGA	PMPSPVPHL		
g165	GGGALTLLQKSGIPEGKGYGGLP	VSGLFFRNSNPETAEOHNAKVY	QASVGA	PMPSPVPHL		
	250	260	270	280	290	300
m165.pep	DTRNVDGKRHLMFGPYAGFRSN	FLKQGSMDLPLSIHMDNLYP	MCLAGWANMPLTK			
g165	DTRNVDGKRHLMFGPYAGFRSN	FLKQGSFMDLPLSIHMDNLYP	MPLRAGWANMPLTKYLLG			
	310	320	330	340	350	360
m165.pep	DTRNVDGKRHLMFGPYAGFRSN	FLKQGSMDLPLSIHMDNLYP	MCLAGWANMPLTK			
g165	DTRNVDGKRHLMFGPYAGFRSN	FLKQGSFMDLPLSIHMDNLYP	MPLRAGWANMPLTKYLLG			
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq  
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC  
 51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC  
 101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC  
 151 AACGCCGGCA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGT  
 201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC  
 251 AGTTTCATGT CAGCCGCCAG TTTTGGCGCA CGTTGGTCGC GGAAGCAAG  
 301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT  
 351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA  
 401 CCCAAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT  
 451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT  
 501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTGATTTC GGACGGCTGA  
 551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGCGTAAA AACCGAGTTC

```

601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACGCG CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTGCCC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAATACTA CCCCAGGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTG GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCCGCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSA LC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWTALVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMRGR DENQPVAA N YSAEGTDVDF GRLTRQMVKY LOGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRELFLLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYGQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPLMRAGWA
351 NMPLTKYLLG ELRKTEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

m165.pep	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSA LC
a165	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSA LC
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
a165	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF
a165	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF
m165.pep	GRLTRQMVKYLOGKGVKTEFNHRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA
a165	GRLTRQMVKYLOGKGVKTEFNHRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL
a165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL

472

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          310      320      330      340      350
m165.pep  DTRNVGDKRHLMFPGYAGFRSNFLKQGS LMDLPLSIHMDNLYPMLCAGWANMPLTK
          |||||
a165      DTRNVGDKRHLMFPGYAGFRSNFLKQGS LMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
          310      320      330      340      350      360

          370      380      390      400      410      420
a165      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

```

g165-1.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGCGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAAGCTCGA ACCGCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT AtgcgccGCT
201 GGGTgcggac ggcgtcatCA ATCCGGCGCG cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctggTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgCTGAT TATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGCGCGG GCGCGCGCGG CACTGACCC TCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCGGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTG GTCCCTTACG
951 AGTTTTCCTT TCCAACTTCC TCAAGCAAGG CTCGTTTATG GATTGCGCG
1001 GTGCCATCCA TATGGACAAC CTCATCCTTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATAA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTtt gCTCCCTGC TGgaatacta cccGaggcag acccGAGc
1151 tggtaactcat cacgcaggnc acGCGTcata tcattanata tgactCgaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgtcgcggcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttggaag gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

```

g165-1.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFNAV PHMSLMVNEH HCRLYQKRYD VFKTKQLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTFLFLGA GGGALTLLQK
251 SGIEGKGYG GLPVSGLFFR NSNPETAQH NAKVYGOASV GAPPMSVPHL
301 DTRNVGDKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYPRQ TRRLVLITQX TRHIXYDSK
401 LRLQLYIEIV PRDARSRIE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

```

m165-1.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGCGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAAGCTCGA ACCGCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATGTCTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCCAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGCGCGG GCGCGCGCGG CGCTGACCC TCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG

```

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851 TGTACGGGCA GGCTTCGTC GCGCGCCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTGCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGTGGGCG GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAAATACTA CCCCAGGAGCA AACCCCGACG
1151 ACTGGGAACAT CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTATTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

```

m165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSAIC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMRGR RDENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVTKEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIEPEGKGYG GFFVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSAIC					
g165-1	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSAIC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165-1	ELNYAPLGADGVINPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
g165-1	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQKGKVTKEFNRHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165-1	GRLTRQMVKYLQKGKVTKEFNRHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIEPEGKGYGGFFVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
g165-1	GGGALTLLQKSGIEPEGKGYGGLPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFPGYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG					
g165-1	DTRNVDGKRHLMFPGYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKGDSEKGGVLQFGTEIVAHADGS					
g165-1	ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKGDSEKGGVLQFGTEIVAHADGS					
	370	380	390	400	410	420
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA  
:  
g165-1 ILERRGASRXALISADDTAPSAPVLESVX  
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq  
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC  
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC  
101 TGATTGAACG CTGGAAGAT GTGGCGTTGG AATCGTCAA CGCGTGAAC  
151 AACCCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAAC ATGCGCGGTT  
201 GGGTGCAAAAT GGGATTATCG ATCCGGGCGC CGCCCTCAAT ATTGCCGAAC  
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG  
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT  
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA  
401 CCCAAAACT TTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT  
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT  
501 CGCCGCCAAC TACTCCGCGC AAGGCACGGA TGTCGATTTC GGACGGCTGA  
551 CGCGCCAAAT GGTGAATAT TTGAGGGCA AGGGCGTAAA AACCGAGTTC  
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT  
651 CAAAACCGCC GATACCCGCA ACCCGACGGC GCAGCTCACC CTCCGTACCC  
701 GCTTCTCTT CCTCGGCGCG GCGGCGCGCG CGCTGACCCT GCTGCAAAAA  
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT  
801 GTTCTTCCCG AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG  
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC  
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCT GGCCTTACGC  
951 AGGCTTCCGT TCCAACTTCC TCAAGCAAGG CTCACATTATG GATTGCGCGC  
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG  
1051 AATATGCCCG TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA  
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGCA AACCCGACG  
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC  
1201 TCCGAAAAG GCGCGTGTT GCAGTTGGT ACGGAGATTG TCGCACACGC  
1251 CGACGGCTCG CTCGCGCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG  
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC  
1351 CCGCTTGGG AAGGCGCTCT GAAAGAGCTG GTACCGGGT ACGCATCAA  
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA  
1451 AAGTGTGGA TATTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep  
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN  
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK  
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI  
151 SDWAPLMMRG RDENQPVAA YSAEGTDVDF GRLTRQMVKY LQGGKVTKEF  
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK  
251 SGIPEKGKYG GFPVSGLFER NSNPETAEOH NAKVYQASV GAPPMSVPHL  
301 DTRNVGKRRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA  
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKID  
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT  
451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI\*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLGVL	LKELEPSWEITLIERLEDVA	LESSNAWNNAGTGHSALC			
m165-1	MAEATDVVLVGGGIMSATLGVL	LKELEPSWEITLIERLEDVA	LESSNAWNNAGTGHSALC			
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
m165-1	ELNYAPLGANGIIDPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAAANYSAEGTDVDF			
m165-1	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAAANYSAEGTDVDF			
	190	200	210	220	230	240

```

a165-1.pep  GRLTRQMVVKYLQGGKGVKTEFNRRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1      GRLTRQMVVKYLQGGKGVKTEFNRRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL
|||||
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
|||||
m165-1      YTAKVLDIX

```

## a165-1/p33940

sp|P33940|YOJH ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION  
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID:o372#5; similar to [SwissProt Accession Number  
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical  
to 490 residues of YOJH ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct  
identical to GB: ECOHU49\_33  
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548  
Score = 458 bits (1167), Expect = e-128  
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVLVLGGGIMSATLGVLKLELEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLILGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

```

```

Query: 63  NYAPLGGANGIIDPARALNIAEQFHVSQRQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSGISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

```

```

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMGRDENQPVAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSLFGRMRYSEDHAQIKAWAPLVMGRDPQKVAATRTEIGTDVNYG 209

```

```

Query: 182 RLTRQMVVKYLQGGKGVKTEFNRRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKSNFSLQLSSEVRALKRNDNTWTVTVADLKNGTAG-NIRAKFVFIGA 268

```

```

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQLVSENPDVVNHHAKVYKASVGAPPMSVPHI 328

```

```

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKRVLFGFPFATFSTKFLKNGSLWDLMSSTTSNVMPMMHVGLDNFDLVKYLVS 388

```

```

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389 QVMLSSEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDSEKGGVLRLGTEVVSDDQGT 448

```

```

Query: 421 XXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

```

P+M+ L+ + F +R +P W+ LK +VP YG KLN + . +  
 Sbjct: 449 IAALLGASPGASTAAPIMLNLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508

Query: 479 IAYTAKVLDI 488  
 + YT++VL +  
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq  
 1 atggcggcgg cggaataaaa acgccccctc gctgtcgatt tccagcacat  
 51 agcgtccggt ctgcacggcg gcatagccgc ttttgcctgc ctgatagggg  
 101 tgcagggcgg aatgcgaaat caggaatca gtcagtttgc cgccgtcttc  
 151 ggcgatattg cccaccagtt tggcaaacaa ggatggcac acgccgtttt  
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg  
 251 acgacggcgt ccaagtcgtt gggatgcttt ccggtcagcc ggacggcggt  
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt  
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta  
 401 ttgtcgatgt atttgacttt gaaaaccggt ttcggcgcg tttgtgccgc  
 451 attttgcggc tgttccggcg tattttcgga tttgcgcag gcggcaagca  
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc  
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg  
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac  
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgt tttgcgcgc  
 701 ctgcctgcaa aatctcttcg atttgcgaag gattagaggt caatgcgttg  
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep  
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF  
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQV GMLSGQPDGV  
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDFDF ENRFRRLCR  
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSOCR LKCRKRGR  
 201 RFRHVVYFN GRMPTASRTL SNNRSLRA FCAPACKISS ICEGLEVNAL  
 251 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq  
 1 ATGGCGCGG CGGAATAAAA ACGCCCCCTC GCTGTGATT TCCAGCACAT  
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT  
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC  
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT  
 201 CTGCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTTGCCG  
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT  
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTGCT  
 351 TGGTTTGCC TTCGCTGCTT TGTCCAAAT CCAAACCGGC AATCGCCGTA  
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC  
 451 GTTTTGCGGC TGTACCGCCG TATTWCGGA TTTGCCGCaC GGCaaRGcAG  
 501 CAGGCAGCCG CCAATACGG CAAAaAwGT wTTCAGCAT CCACaYTCCT  
 551 GATGGTTTCA AATGCCGTC TGAACCGCG CAGGCGGAGG TTCGGACGGC  
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA  
 651 ATAATTCGCG TGCTTCTTA CGCGCTTTCG CCGCGCTGC CTGCAAAATC  
 701 TCTTCGATT GCGAAGGGTC GCGGTCAGC TCCTTGTA

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep  
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN \*VIRQFAAVF  
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI  
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRLYR  
 151 VLRLYRRIxG FAATAXQQA AQYKXXXQH STXLMVSKCR LKRGRRRFGR  
 201 HRVHFNGRMP TASGTLNNNS RASLRAFAAP ACKISSICEG SAVSSL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng)

from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
	:					
g204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMRNQVISQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
	:       :					
g204	GMAHAVFRPARRRVL SVGFHTFADDDGFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNRRIVDIYDFENRFRRALYRVLRLYRRIXGFAATAXQQAQAQYKXXXQH					
	:					
g204	FATLSQSQTGNRRIVDVDFENRFRRALCRILRLFRRI FGFAAGGKQQAQAQHGKRYFQH					
	130	140	150	160	170	180
	190	200	210	220	230	
m204.pep	STXLMVSKCRLK---RGRRRFGRHRVHFNRMPTASGTLNNSRASLRAFAAPACKISS					
	:					
g204	SALLMVSKCRLKCRLKGRRRFGRHWVYFNRMPTASRTLSNNSRASLRAFCAPACKISS					
	190	200	210	220	230	240
	240					
m204.pep	ICEGSAVSSLX					
	::					
g204	ICEGLEVNAL					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204.seq

```

1  ATGGCGGCGG CGGAAATAAA ACGCCCCCTC GCTGTCGATT TCCAGCACAT
51  AGCGTCCGTT CTGCACGCGC GCATAGCCGC TTTGCGCTGC CTGATAGGGT
101 TGCAGGCGCG AATGCGAAAT CAGGTAATCC GTCAGTTTGC CGCCGTCTTC
151 GCGCATATTG CCCACCAAGT TGGCAAACAA GGTATGGCAC ACGCCGTTTG
201 CCGCCACAGC CGAAGGCGCG CCCTTTCCGT CGGTTCCAT ACATTTGCCG
251 ACGACGGCTT CCAAGTCGTT GGGATGCTTG CCGGTCAGCC GGACGACGTT
301 TTGTTCCGGC AAGCCTTT.. .....
351 .....
401 .....
451 .....
501 .....
551 .....AAGAG GTTCGGACGG
601 CATTGGGTTT ATTTCAACGG GCGGATACCG ACCGCATCAC GTACTTTGCC
651 CAATAATTCG CGTGCTTCTT TACGCGCTTT TTGCGCGCCT GCCTGCAAAA
701 TCTCTTCGAT TTGCGAAGGG TCGGCGGTCA GCTCGTTGTA G

```

This corresponds to the amino acid sequence &lt;SEQ ID 702; ORF 204.a&gt;:

a204.pep

```

1  MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVIRQFAAVF
51  GDIAHQFGKQ GMAHAVCRPA RRRALSVGFH TFADDDGFQVV GMLAGQPDVV
101 LFRQAF....
151 .....KRFRGR
201 HWVYFNGRIP TASRTLPNNS RASLRAFCAP ACKISSICEG SAVSSL*

```



**m204/a204 54.5% identity in 246 aa overlap**

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLAQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVMGFHTFAADGFQVAGMLAQSDNILFRQAFNRITDLFFAVVGFA					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQGTGNRRIVDIYDFENRRFRALYRVLRLYRRXGFAATAQQAAAQYKXXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKGRRRFRHVRHFNRMPTASGTLNNSRASLRFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNSRASLRFAAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcggaaca tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 ggcgcgcgaa accggttttc aaagtaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgctcg cggcaaatgt
301 atggaaaccg acggaaagga cgcgccttcg ggctggcgcg aaaacggcgt
351 gtgccatacc ttgtttgcca aactgggtgg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgcctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgacag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccgcat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNTA EDGGKLTDL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAaAw CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGGCAAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CGGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGA TTTGGGACAA AGCAGCGAAG GCAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGA AGCCGTCAGC GGCAAATGTA
301 TGGAaACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTtTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTGCGATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

**m205/a205 88.3% identity in 111 aa overlap**

a205 88.5% identity in 111 aa overlap  
 50 60 70 80 90 100  
 m205.pep KVIYIDNTAIAGLDLGQSSEGTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC  
 | : ||||| : || ||||| : ||  
 a205 SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC  
 10 20 30  
 110 120 130 140 150 160  
 m205.pep METDDKDSPAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

This corresponds to the amino acid sequence <SEQ ID 710; ORF 205-1.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 711>:

This corresponds to the amino acid sequence <SEQ ID 712; ORF 205-1>:

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSAKPVPVKVYIDNTA	IAAGLALGQSSE				
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPQNAVQSAKPVPVKVYIDNTA	IAAGLDLGQSSE				
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKGKQISYPYIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKD	APSGWAENGVC	HT			
m205-1	GKTNDGKGKQISYPYIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDS	PAGWAENGVC	HT			

481

```

              70      80      90      100     110     120
              130     140     150     160     170
g205-1.pep    LFAKLVGNI AEDGGKLT DYLSH SALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
              |||
m205-1        LFAKLVGNI AEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
              130     140     150     160     170     180
m205-1        YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TTCGGGCTGG GCGGCAACG GCGTGTGCCA TACCTTGTTT
151 GCCAACTGG TGGGCAATAT CGCCGAAGAC GCGGGCAAAC TGACGGATTA
201 CCTGATTTCG CATTCGCCCC TGCAACCTTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTATT TCCGCCGCCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKCM ETDGKGAPSGW AANGVCHTLF
51  AKLVGNIAED GGLTDYLI S SALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep    KYIDNTA IAGLDL GQSSEK TNDGKK QISYP IKG LPEQNVIR LIGKHP GDLEAV S GKCME
              |||
a205-1        PLKGLPEQNVRLTGKHPNDLEAVVGKCM E
              10      20      30
              110     120     130     140     150     160
m205-1.pep    TDDKDS PAGAENG VCHTLF AKLVGNI AEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNG
              |||
a205-1        TDGKGAPSGWAANGVCHTLF AKLVGNI AEDGGKLT DYLSH SALQPYQAGKSGYAAVQNG
              40      50      60      70      80      90
              170     180
m205-1.pep    RYVLEIDSEGAFYFRRRHYX
              |||
a205-1        RYVLEIDSEGAFYFRRRHYX
              100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc ccgacaaaac ctttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctccgactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgcctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 gcccgcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcatccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttgga gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng)

from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCTCT TGTCTCAGCG CACTGCTCCT
   CGCCTCATGG GGCACGACCT CCGGCAAAAC CCGCCAACCG AAACCCCAAAC
101 AGACAGTCCG GCAAAATCCAA GCGCTCCGCA TCAGCCACAT CGACCGCACA
   CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGACGCGC
201 CTACAAATGG GCGGGGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
   TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCGCGCGACC
301 GCGCGCGACA TGGCGGCGGC AAGCGCAAAA ATCCCCGACA GCGCGCTTAA
   GGCGGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTACAC
401 ACGTCGGACT CTATATCGGC AAGGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACGTTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQAVRISHIDRT	QGSQELMLHS			
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQAVRISHIDRT	QGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYK	NALNVKLPRTARDMAAASRK	IPDSRXKAGD		
a206	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYK	NALNVKLPRTARDMAAASRK	IPDSRLKAGD		
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGN	GEFIHAPSSGKTIKTEKLST	PFYAKNYLGAHTFFTEX			
a206	LVFFNTGGAHRYSHVGLYIGN	GEFIHAPSSGKTIKTEKLST	PFYAKNYLGAHTFFTEX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttggcgcgct tgttttcga
51  tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcggttcag ataggtttg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcadc gcttgctgtt gcgccatacg
451 gtcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcgccac
501 gcattttcgc catcgaacgg taggagcggt tggatcaatg atacgtacg
551 gctttgacga tgatggtcaa aacgacgatt gcccagcccc agttgcccgt
601 aatgtgtgac agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctggc gatgtttgcg
701 ataacggatg tggtttgccg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cggttgggg tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEHEDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCFVQADEDG DLQQRQTAA QRVDFLVFEK LHHRLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEPE ERRCEPVYFT VVFCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAAGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTCGCC TGCATCGGCT CGGTCGGCGG
201 CGGTTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGCGGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTCGGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGCTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGAGAAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTGCGGG TTTTGCAGAT GTATTGCGCC
951 TCGGATTTCG CGGATTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFALGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDQDQVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDLQQHRQAAA QRVDFLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTVLVLSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng)

from *N. gonorrhoeae*:

m209/g209

m209.pep	10	20	30	40	50	60
	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR					
g209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEEHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	70	80	90	100	110	120
	LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDGDL					
g209	LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAAEVGNPAQPRCLAQFYGGEQCPVQADEG					
	70	80	90	100	110	120
m209.pep	130	140	150	160	170	180
	DLQQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW					
g209	DLQQHRQTAAQRVDFLVFEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGVGVGQW					
	130	140	150	160	170	180
m209.pep	190	200	210	220	230	240
	IQYGFDDGDXNDNRPAPVADDVVQLVQEP EERGEPVYFAVVFGQLQVVGQDVCDGCGLR					
g209	IQYGFDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVCQLQVVGQDVCDGCGLR					
	190	200	210	220	230	240
m209.pep	250	260	270	280	290	299
	AGVEVDGGFGF-APFWMAAKGTLTLVLVLSLRLMSMLHSPAAQTLCLPLGWRIQVDMK					
g209	TGIQVDRHFRFWPPGWDSG					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

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```
51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101  ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151  AACCAGGTCAG ATAGTTTTCG TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201  GCGGGTTCAG ATAGTTTTCG GCGAACATCG TTGCCGCCAT AATGATGGGC
251  AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301  AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351  TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401  ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGTCT GCGCCATACG
451  GTCGTCGCGG TATTCTCTTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501  GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551  GCTTTGACGA TGATGGTTAA AACGATAATC GCCAGCCCC AGTTGCCGAT
601  GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCACT
651  GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGGC GATGTTGCG
701  ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751  TTCGACCGGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGTCTGA
801  CAGCTTGTGC TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851  AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901  TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTTGGCGA TGTATTCGGC
951  CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```
a209.pep
1  MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51  NQRHDFHHER LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101  RCLAQFYGGE QCPIQSDGDL DLQQRQAAA QRVDFLVCVK LHHGLLLRHT
151  VVAVFLFDGL QFGRGGTHER HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201  DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNCGCLW AGVEVDGGFG
251  FAPFWIAAKG TLTLVLYSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301  CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*
```

m209/a209 95.6% identity in 341 aa overlap

```
10 20 30 40 50 60
m209.pep MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGENQRHDFHHER
|||||
a209 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGENQRHDFHHER
10 20 30 40 50 60

70 80 90 100 110 120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG
|||||
a209 LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG
70 80 90 100 110 120

130 140 150 160 170 180
m209.pep DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||
a209 DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRTVRGVGQW
130 140 150 160 170 180

190 200 210 220 230 240
m209.pep IQYGFDDDGXNDNRPAVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR
|||||
a209 IQYGFDDDGXNDNRPAVADDVVQLVQKPEGGGEVYFAVVFGQLQVVGDVCDGCGLR
190 200 210 220 230 240

250 260 270 280 290 300
m209.pep AGVEVDGGFGFAPFWMAAKGTLTLVLYSLSLRRLMSLHSPAAQTLCLPLGWRIQVDMKW
|||||
a209 AGVEVDGGFGFAPFWIAAKGTLTLVLYSLSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW
250 260 270 280 290 300

310 320 330 340
m209.pep CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX
```



```

|||||
a209      CSIMPSQPVGVLRMYSASDLPLDASSKSEKLTFWKLP SGVX
           310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttggcgg tgggtgctgat aatcaggttg
101 agtttttggg aggaaacctg attgtagtcg gcgcgtccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgcgcgccgc gtttttgtcc
251 tgttcgcgca ggaacaggtt tttcatgatg ccggattcgg tgtcaaaggt
301 ttcgacgaaa taaaccctgc cgttgcgctt gcccaagtta ttgaactcgc
351 cggcttccac caaagacaat tcctgcttct gtttcaaaat ttcggcatat
401 tcgcggctgc gcagctctgc ccacggatc acccaaagct gcatgacggc
451 aatcaggatg gcaaacggca cggcaaaact catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatat

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1  MLRIAAANQL GGRNGAAVGN GVDKFRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFQEQV FHDAGFGVKG
101 FDEINPAVAL AQVIELAGFH QRQFLLLQN FGIFAAALC PRYHPKLHDG
151 NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTGCGATG AGTTTGGCGG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGGG AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTG TCCTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTCGCGGCC GTTTTGTCC
251 TGTTCGCGCA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAA TAAACCCTGC CGTTGCGCTT GCCCAAAGT TTGAACCTCG
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAACCGGCA CCGCAAAGT CATCACGGG CGTATCCATT
501 GTTCAATGC CAATCCGCA GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1  MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QRQFLLLQD FSVFAAAXLC PRYHPKLHDG
151 NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211
           10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211       MLRIAAANQLGGRNGAAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
           10      20      30      40      50      60
           70      80      90     100     110     120
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 731>:

This corresponds to the amino acid sequence <SEQ ID 732; ORF 211.a>:

m211/a211 99.4% identity in 174 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 733>:

g212.seq (partial)

1	atggacaatc	tcgtatggga	cggcattccc	gacatccgca	cactcgacca
51	aaatcatccg	aaacacgcac	acccgctcaa	cctgattgtc	tgccctcccc
101	ataactcagat	tcccgatttt	caaacgcgac	aagatgtctc	ggactcggaa
151	tgccgtctga	agcaccggtt	ggatcaggca	accagtgcc	ttcagttcga
201	cagcatcaac	ctcatcgaac	acatcctgcc	cgatgtccgc	ttctggctgg
251	ttcccccttc	agcgaacccc	cgactgcacg	aacatttcca	cccatatttc
301	tggcagaccg	aagccatccc	gcaaacgcga	agcaagtccg	acaaacctcg
351	gtttgcactt	ccacaaacat	ccgaacggaa	aaaaccggaa	cacgtcctcg

```

401 tcatcggtgc aggcattgcc ggcgcatcga ccgcccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaatctcgc ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctcggacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacggcg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcacctcctc cagccatccg ctgatcgaa tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaaccte gccgccctac ccctcaggca aatacgcgga
1051 caaacggcc tcacaccgtc caccctgtt tccgaacaac tgcgttgcgc
1101 cgtttcaggc gaaagctaca tcagcccgct gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcga agcattggca cacttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQITR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RIHEHFHHIS
101 WTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCT CCACATTTC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GCGCGGGCAA CCGCCACGCG CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CACGGGCAAC CGCAAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACACA TCCTGCCCCG ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTGCTCC
851 GCACCCTCCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATT CCCACGACGG GGAaaAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TCGGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCAT TGTTGCCGCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGACACACC TTCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAACCTACCG ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGACTCGCCA CCGCCCCAT CTGCGCGGCC

```

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1501 GmCAwTGcAG CCCAAATCaT AGGcYTGCCC CATCCCTTTT yAcAAcGCCT  
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA  
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep  
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE  
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS  
 101 WQTEAIPQTE SKPDKPFAL POTSERQKPE HILVIGAGIS GAATAHALAS  
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL  
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA  
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL  
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG  
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA  
 401 EEASNRQALA HLNPALESSE FAANPNQKH QGHAAIRCDS PDHLPLVGAL  
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLEN AYVNTAHGTR GLATAPICAA  
 501 XXAAQIXGLP HPFXQLRHA LHPNRTIIRA IVRKDLTP\*

Computer analysis of this amino acid sequence gave the following results:

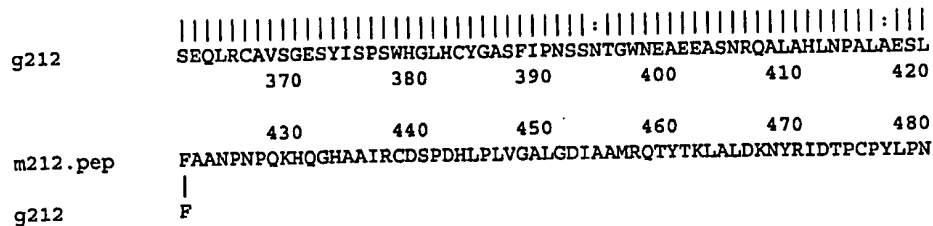
Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng)  
 from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII CLPDNQIPDFQTAQDASDAECRLKHLRDQA					
g212	MDNLVWDGIPDIRTLDQITRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRKHLRDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKPFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	PQTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEASNRQALAHLPALSESSE					

490



-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

a212.seq

1	ATGGACAATC	TCGCATGGAA	CGGCATTCCC	GACATCCGCA	CACTCGACCA
51	AACCATCCGC	AAACACGCAC	ACCCGCTCAA	CCTGATTGTC	TGCCTCCCCG
101	ATAATCAGAT	TCCCAATTTT	CAAACCGCAC	AAGATGCTTC	GGACGCGGAA
151	TGCCGTCTGA	AGCACCGTTT	GGATCAGGCA	ACCCAGTGCC	TCCAGTTCGA
201	CAGCATCAAC	CTGATTGAAC	ACATCCTGCC	CGATGTCCGC	TTCTGGCTGG
251	TTCCCCCTTC	ACGCACCCGC	CGCCTGCACG	AACACTTCCA	CCACATTTC
301	TGGCAGACCG	AAGCCATCCC	GCAAACCGAA	AGTAAGCCCG	ACAAACCTTG
351	GTTTGCACCT	CCACAAACAT	CCGAACGGCA	AAAACCGGAA	CACATCCTCG
401	TTATCGGAGC	GGGCATATCC	GGCGCGGCAA	CCGCCACGC	CTAGCATCA
451	TACGGCATT	CCGTTACCGT	ATTGGAAGCC	CGAAAAGCCG	CCCAAGCCGC
501	CAGCGGCAAC	CGCCAAGGGC	TGCTCTACGC	CAAAATCTCG	CCGCACGACA
551	CCGAACAAAC	CGAACTGCTG	CTTGCCGGCT	ACGGCTACAC	CAAACGCCTG
601	CTCGGACATA	TCCTGCCCGA	ATCCGAAACC	TGGGGCGGCA	ACGGCATCAT
651	CCACCTCAAT	TACAGCCGCA	CCGAACAACA	ACGCAATCAC	GAATTGGGTT
701	TGCAAAAACA	CCATAACCAC	CTCTACCGCA	GCATCACGCA	GGCAGAAGCC
751	GAAAAAATCG	CCGGCATCCC	TCTGAACACG	CCCTACGCCG	AACCATTATG
801	CGGACTGTTT	TGGCAGTACG	GCGTATGGCT	CAATCCTCCC	ACATTCTGTC
851	GCGCCCTCCT	CAGCCATCCG	CTCATTGGAC	TACACGAAGA	CACACCGTTA
901	ACCGACATTT	CCCACGACGG	GGAAAAGTGG	ATTGCAAGCA	CGCCAAACGG
951	CACATTTACC	GCCACACACA	TCATCTACTG	CACCGGTGCG	AACAGCCCTT
1001	ACCTACCCGA	AACCAACCTC	GCCACCCTGC	CCCTCAGGCA	AATACGCGGA
1051	CAAACCGGCC	TCACACCGTC	CACCCCGTTT	TCCGAACAAC	TGCGTTGCCG
1101	CGTTTCAGGC	GAAAGCTACA	TCAGCCCGTC	GTGGCAGGGA	CTGCACTGCT
1151	ACGGCGCGAG	TTTTATTCCC	AACAGCAGCC	ATACCGGATG	GAACGAAGCC
1201	GAAGAAGCCT	CAAACCGCCA	AGCATTGGCA	CACCTTAACC	CCGCCCTTTC
1251	CGAATCATTG	TTTGCCGCCA	ACCCAAACCC	CCAAAAACAC	CAAGGGCAGC
1301	CCGCCATACG	CTGCGACAGC	CCCGACCACC	TTCCCTTAGT	CGGCGCACTC
1351	GGCGACATTG	CCGCTATGCA	ACAAACTTAC	GCCAACTCG	CGCTGGACAA
1401	AAACTATCGC	ATCGATGCCC	CCTGCCCGTA	CCTGCCCAAT	GCCTACGCCA
1451	ACACCGCCCA	CGGCACACGC	GGGCTTGCCA	CCGCCCCCAT	CTGCGCCGCC
1501	GCCGTTGCAG	CCGAAATCCT	AGGCTTGCCC	CATCCCTCT	CAAAACGCCT
1551	GCGCCACGCC	CTACACCCCA	ACCGCGCCAT	CATCCGCGCC	ATCGTCAGAA
1601	GGAAGGATCT	AACCCCTTAA			

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

a212.pep

1	MDNLAWNGIP	DIRTLDQIR	KHAHPLNLIV	CLPDNQIPNF	QTAQDASDAE
51	CRLKHLRDLQA	TQCLQFDSIN	LIEHILPDVR	FWLVPPSRTR	RLHEHFHHIS
101	WQTEAIPQTE	SKPDKPWFAL	PQTSERQKPE	HILVIGAGIS	GAATAHALAS
151	YGISVTVLEA	RKAAQAASGN	RQGLLYAKIS	PHDTEQTELL	LAGYGYTKRL
201	LGHILPESET	WGGNGIIHLN	YSRTEQQRNH	ELGLQKHHNH	LYRSITQAEA
251	EKIAGIPLNT	PYAEPLCGLF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL
301	TDISHDGEKW	IATPNGTFT	ATHIIYCTGA	NSPYLPETNL	ATLPLRQIRG
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGFIP	NSSHTGWNEA
401	EEASNRQALA	HLNPALSESL	FAANPNPQKH	QGHAAIRCD	PDHLPLVGAL
451	GDIAAMQQTY	AKLALDKNYR	IDAPCPYLPN	AYANTAHGTR	GLATAPICAA
501	AVAAEILGLP	HPLSKRLRHA	LHPNRAIIRA	IVRRKDLTP*	

m212/a212 93.7% identity in 539 aa overlap

	10	20	30	40	50	60
m212.pep	MDNLVWDGIP	DIRTLDQAIRK	HAPLNLIICLP	DNQIPDFQTAQ	DAECRLKHLRDLQA	
a212	MDNLAWNGIP	DIRTLDQIRK	HAHPLNLIVCL	PDNQIPNFQTAQ	DAECRLKHLRDLQA	

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	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctatttggt ttaattgtaa tttttgcaac
51  ttctcccget tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagctc aacatttcg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag ggcggaagg
251 tcgcccgtcc gcttcagcca aacgttgga gggggcaag ggacggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagt cagcgcggcg gcgacgttgc cgaagggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

492

```

1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQRTTFS
51  GNVIIROGTL NISASCVNVT RGRQRRRIRE GGRFARPLQ NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQROH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTACGCCAG ACATTGGACG GCGGCAAAGG CACGGTGC GC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLFV LIAFFSASPA FALQSDSROP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAA RVNVT RGRQRRRIRE GGRFASPLQ DIGRRQRHGA
101 RTGKQRC LFI CRQHRSLNR* CQSTARRRCR RRCGDIYI HQ NRSLYHQROH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng)

from *N. gonorrhoeae*:

m214/g214

	10	20	30	40	50	60
m214.pep	MIQKICKLFVLIAFFSASPALQSDSRPIQIEADQGS LDQANQSTTFSGNVVIRQGT L					
	:     : : :     :     :     :     :     :					
g214	MIQKICKLFVLIVIFATSPALQSDSRRPIQIEADQGS LDQANQRTTFSGNVIRQGT L					
	10	20	30	40	50	60
m214.pep	70	80	90	100	110	120
	NISAA RVNVTGRQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRC LFI CRQHRSLNRX					
	:      :     :     :     :     :     :     :     :					
g214	NISASCVNVTGRQRRRIREGGRFARPLQPNVGRGQRDGARS GKQRYLFLRRKHCRSDRQ					
	70	80	90	100	110	120
m214.pep	130	140	150			
	CQSTARRRCRRRCGDIYI HQNRSLYHQROHKI					
	:             :     :     :     :					
g214	CQSAARRRRCRRRCGHYLQHQNRSLYHQROHEIGCEIRFQNRQGQRRHPAFKHTKNRITPM					
	130	140	150	160	170	180
g214	PSETETQFRRHLPTEMPRRDY					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGCGGCGC AATCCGTGAG GCGGGAAGGT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

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```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNV T RGXQRRRIE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRC LFI CRQHRSLNR* CQSTARRRC R RCGDYIQH Q NRSLYHQ RQH
151 KIRRKIRFQ I RQGRRYPAF EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
a214	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
	10	20	30	40	50	60
	70	80	90	100	110	120
m214.pep	NISAARVNV TRGRRRIE GGRFASPLQ PDIGRRQRH GARTGKQ RCLFICRQ HRS LN R X					
a214	NISAARVNV TRGRRRIE GGRFASPLQ PDIGRRQRH GARTGKQ RCLFICRQ HRS LN R X					
	70	80	90	100	110	120
	130	140	150			
m214.pep	CQSTARRRC RRCG DYIQH QNRS LYHQ RQH KI					
a214	CQSTARRRC RRCG DYIQH QNRS LYHQ RQH KIRRKIR FQIRQG RRYPAF EYAKIRI IP M					
	130	140	150	160	170	180
a214	PSETXTWFG RHLPTEILKRY L X					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
51  TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTTCG CCTCGCGCGT
201 CAACGTCACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGT
251 CGCCCGTCCG CTTACGCCAA ACGTTGCAGC GGGGCAAGG GACGGTGCGC
301 GGTCAAGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CCGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISARVNV T RGGKGGSVR AEGSPVRF S Q TLDGGKGTVR
101 GQANNVTYSS AGSTVVL TGN AKVQRGGDVA EGAVITYNT K TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCGT

```



494

```

201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

```

m214-1.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
151 KSGAKSASKS GRVSVVIQPS STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

```

m214-1.pep      10      20      30      40      50      60
MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS L DQANQSTTFSGNVVIRQGT L
|||||:|||||:|||||:|||||:|||||:|||||
g214-1          10      20      30      40      50      60
MIQKICKLFVLIVIFATSPAFALQSDSRRIQIEADQGS L DQANQSTTFSGNVIRQGT L
|||||:|||||:|||||:|||||:|||||:|||||

m214-1.pep      70      80      90      100     110     120
NISAARVNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGT VRGQANNVAYSSAGSTVVLTGN
|||||:|||||:|||||:|||||:|||||:|||||
g214-1          70      80      90      100     110     120
NISASRVNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGT VRGQANNVTYSSAGSTVVLTGN
|||||:|||||:|||||:|||||:|||||:|||||

m214-1.pep     130     140     150     160     170
AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKS GRVSVVIQPSSTQKSEX
|||||:|||||:|||||:|||||:|||||:|||||
g214-1         130     140     150     160     170
AKVQRGGDVAEGAVITYNTKTEVYTINGSTKSGAKSASKTGRVSVVIQPSSTQKTEX
|||||:|||||:|||||:|||||:|||||:|||||

```

g214-1/p38685

```

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_0185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

```

```

Query: 19  PAFALQSDSRQPIQIEADQGS L DQANQSTTFSGNVVIRQGT L NISAARVNVT R--GGKGG 76
          PAF+  D+  QPI IE+DQ SLD      TF+GNV++ QGT+ I+A +V VTR G +G
Sbjct: 24  PAFAVTGD TDQPIHIESDQQLDMQGNVVTFTGNVIVTQGTIKINADKV VVTRFGGEQ GK 83

Query: 77  ESVRAEGSPVRF SQ TLDGGKGT VRGQANNVAYSSAGSTVVLTGN AKVQRGGDVAEGAVIT 136
          E +  G P F Q D GK V G A+ + Y A VVLTGNA +Q+ +G IT
Sbjct: 84  EVIDGYGKPATFYQM DNGK-PVEGHASQMHYELAKDFV VLTGNAYLQ QVDNSIKGDKIT 142

Query: 137 YNTKTE 142
          Y K +
Sbjct: 143 YLVKEQ 148

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

```

a214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTACGC
151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

```

a214-1.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGTVR  
101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST  
151 KSGAKSASKS GRVSVVIQPS STQKSE\*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLIAFFSASP	AFALQSDSRQPIQIEADQ	GSLDQANQSTTFSGNV	VIRQGTI		
m214-1	MIQKICKLFVLIAFFSASP	AFALQSDSRQPIQIEADQ	GSLDQANQSTTFSGNV	VIRQGTI		
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGESVRAEGSPVR	FSQTL	DGGKGTVRGQANNV	AYSSAGSTVV	LTGN
m214-1	NISAARVNVT	RGGKGGESVRAEGSPVR	FSQTL	DGGKGTVRGQANNV	AYSSAGSTVV	LTGN
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVAEGAVITY	NTKTEVYTISGSTKSGA	KSASKSGRVS	VVIQPSSTQKSE		
m214-1	AKVQRGGDVAEGAVITY	NTKTEVYTISGSTKSGA	KSASKSGRVS	VVIQPSSTQKSE		
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq  
1 atgaaagtaa gatggcggta cggaattgcg ttccattga tattggcggg  
51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa  
101 tcgagggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc  
151 ttggacggaa ggcggtttga cgaacagggg tacttgaaag aacatttgag  
201 cgcgaaaggt gcgaaacagt ttcccgaata cagcgacatc cattttgatt  
251 cgccgcattc cgtgttcttc caagaaggca ggctgttgta cgaagtcggc  
301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc ttttataaaa  
351 caacgttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaa  
401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaac  
451 gatacgcttg tcagtttcca atatggcgcg tcgcacgggc aggcgggcgg  
501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga  
551 aagccgcgat ttatgataca aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep  
1 MKVRWRYGIA FPLILAVAG SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS  
51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPHLVFF QEGRLLYEVG  
101 SDEAVYHTEN KQVLFKNVNV LTKTADGRRQ AGKVETEKLH VDTESQYAQT  
151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)  
1 ..AGCCTGTCGG CATGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT  
51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA  
101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGCG  
151 GCGAAACAGT TTCCGAAAAG CAGCGACATC CATTTTGATT CGCCGCATCT  
201 CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG  
251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG  
301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA  
351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG  
401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC  
451 GACCACAWWA CAGGCATGTT GAATTCTCA TCTAAAGTGA AAGCCACGAT  
501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)  
1 ..SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG  
51 AKQFPENSDI HFDSPHLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNVNV  
101 LTKTADGRRQ AGKVEAEKLH VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

496

151 DHXTGMLNFS SKVKATIYDT KDM\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

```

      10      20      30      40
m215.pep      SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
               |||||:|||||
g215      MKVRWRYGIAFPLILAVLGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
               10      20      30      40      50      60

               50      60      70      80      90      100
m215.pep      YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
               |||||:|||||
g215      YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
               70      80      90      100      110      120

               110      120      130      140      150      160
m215.pep      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSPFYQASHGQAGGMTYDHXTGMLNFS
               |||||:|||||:|||||
g215      LTKTADGRRQAGKVEAEKLHVDTESQYAQTDTPVSPFYQASHGQAGGMTYNHKTGMLNFS
               130      140      150      160      170      180

               170
m215.pep      SKVKATIYDTKDMX
               |||||:|||||
g215      SKVKAATYDTKDM
               190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

```

a215.seq
1  ATGAAAGTAA GATGGCGGTA CGGAATTGCG TTCCCATGTA TATTGCGGTA
51  TGCCTTGGGC AGCCTGTCGG CATGGTGGG ACGCATCAGC GAAGTCGAGA
101 TTGAAGAAGT CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACGGA
151 TTGGATGGCA GCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG
201 TTCGAAGGGC GCGAAACAGT TTCCCGAAAG CAGCGACATT CATTTCGACT
251 CACCGCATCT CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC
301 AGCGATGAAG CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA
351 CAACGTTGTG CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG
401 TTGAAGCCGA AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC
451 GATACGCCTG TCAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG
501 CATGACTTAC GACCACAAA CAGGCATGTT GAACCTCTCA TCTAAAGTGA
551 AAGCCACGAT TTATGATACA AAAGATATGT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 756; ORF 215.a&gt;:

```

a215.pep
1  MKVRWRYGIA FPLILAVLGS SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
51  LDGRRFDEQG YLKEHLSSKG AKQFPESDI HFDSPHLVFF QEGRLLYEVG
101 SDEAVYHTEN KQVLFKNNVV LTKTADGKRQ AGKVEAEKLH VDTESQYAQT
151 DTPVSFYQGA SHQAGGMTY DHKTGMLNFS SKVKATIYDT KDM*

```

m215/a215 98.3% identity in 173 aa overlap

```

      10      20      30      40
m215.pep      SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
               |||||:|||||
a215      MKVRWRYGIAFPLILAVLGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
               10      20      30      40      50      60

               50      60      70      80      90      100
m215.pep      YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV

```

497

```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
              70      80      90      100      110      120

              110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHTGMLNFS
              |||||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHTGMLNFS
              130      140      150      160      170      180

              170
m215.pep  SKVKATIYDTKDMX
              |||||||
a215      SKVKATIYDTKDMX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtacccagc gacgaaatca cgcgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgc
101 ccgattcaac catggcgcg ccatgccgata tccacatcac cgcacggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgcccg cagcctcgcc
301 aaacgcctgc ttttgcgctg tgcgcacatt atgcacaaag gcggcgccct
351 gcccgcctgc cgactcggca cgccttgaa aggagccatc gtcagcatga
401 gcgagaaaagg tttgggcatg tggcggggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGAACAAA
101 ACTTCGTCTT TGCGGCAGAC GCGTTGTGTC ACTGCAAGGG CAGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGCGACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGA TTTGGGTATG ATTGTGGACA rGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCAGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGGCGCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCT TCCTGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTTCG CTTGAGCCAT CCTGCCGSCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CTTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLEIRIAE LXKNFVLAAD ALLHCKGRV

```

```

51 ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLMG IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng)

from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100     110     120
m216.pep      TMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVCI
              ::|||:| ||||:|||||||
g216          MISISSVPSDEITAIIPALKRKDITLVCI
              10      20      30

              130     140     150     160     170     180
m216.pep      TARPDMSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g216          TARPDMSTMARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              40      50      60      70      80      90

              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g216          ALIHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKGAIVSMSEKGLGMLAVTDGQRL
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

a216.seq

```

1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51  GCACACCGAA GCGGAAGGCT TGCGCGAAT TGCGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGCGGAC GCGTTGTGTC ACTGCAAAG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAA TGCGGGCAAC
201 CATGGCCTCG ACCGCGACGC CCGCGTTTTC CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCCG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCAGCCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCC
551 ACGACTTCGC CTGAGCCAC CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCTGCG CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

a216.pep

```

1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRV
51  ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLMG IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN

```

301 GLLVTDADGV LIGALNMHDL LAARIV\*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENGKYLDWAREVLHAAEAGLREIAAELXKNFVLAADALLHCKGRVVITGMVKSCHI					
a216	MAMAGNEKYLDWAREVLHTEAAGLREIAADLDENFALAADALLHCKGRVVITGMGKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRCLKGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN					
a216	DGQGRCLKGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGV LIGALNMHDL LAARIVX					
a216	GLLVTDADGV LIGALNMHDL LAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttgtt gcggaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctgaggtt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga cgtcgcagg ttgccccat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcgggtt
251 tgattcacgt cggcatacca cgcgctgaca tctgcccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgccgcgca tttctccgtc caatccccc
401 tggacgttca aatcggaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgc aaacggcgca acacgggcgc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcaactccaac
551 gcataaaaaa acgggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgtata gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAQQQVGH ALQRIKKRLP AADFHVNRGI

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

82	1	ATGGCGGATG	ACGGTGTGCG	GCGGCAACTG	TCCGGA AAAA	TGCGCCAATT
51		CGGTTTCCCG	CTrCCATTTG	ACCCATTTCG	TTTCAAGGTT	TTGGCATGAC
101		TTTTTGTCAT	CGGCTTCGAG	TTGGAAACAT	GTTTCAAGCA	AATCCCGGCA
151		ACGCGCCACC	CATTCTCCGA	CCGTGTGCGG	GTGCGCCCAT	ATCCGTACAA
201		TATCCGTCAG	GGTTTCGAGG	AAGGCGGC AA	AACGTCCGAA	CATGGCGGTT
251		TGATTACAGT	CGGCATACCA	CGCGCTGACA	TCCTGCCACA	TCGGATTGCC
301		GCCTTTGGGC	AGCATCCAGC	CCAATATCAT	GC GTTCTACC	GCTGTGTTCC
351		AGGTGAACAG	CTGATCCGTG	CCGCGCGCGA	TTTCTCCGTG	CAAAACCCAG
401		TGGACGTTCA	AATCGGCAAC	CATGTCTGTG	AAAGCGGATA	AATCGTCTCT
451		AGTCAGTCCG	AAACGGCGCA	ACACGGGCGC	GGTTTCTAAA	AGCACAAAGCA
501		CTTTATCGAC	TTCAAATCGG	CTTTCAACA	AGTCGAACAG	GCATGACAAA
551		GCATGAAACA	GCGGTTGCGG	GCGGCTGACT	TTACAGTCTG	ACACGGAATA
601		CGGCAATGCC	TGCGCATCCG	GctGCGCGTT	TCCGAACACG	GCTTCGATAA
651		AAGGCGTGATA	GATTTCGATA	TTCGGGTTA	A	

m217.pep

```

1 pep
1 MADDGVRRLQ SGKLRQGFGR LPFDPVFVKV LDXLLLVIGFS LEQCFKQIPA
51 TRHPFADRCG LPPYPYNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFVS QTPVDVQIGN HVVQKRXIVL
151 SQSETAQHGR GFXKKKHKFID FKSAFQQVEQ AQXSMKQRLA AADFHVXHGL
201 RQCLRTGLRL SEHGFDKKRI GFDIRG*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLQSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHHPFADR	CG				
	:				:	
g217	MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHHPFADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA	AFGQHPAQYHAFYRLLPGEQ				
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA	AFGQHPAQYHTVCRLLPGKQ				
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFQKXKH	FIDFKSAFQQVEQ				
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRIQVPGQSETAQHGRGFQKREHFADFKTAFQQVG	H				
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
			:	:		:
g217	ALQRIKKRLPAADFHVRNGIRQCLRAGLRRLSEHGFGHKKRIGFDIRG					
	190	200	210	220		

a217.seq

1 GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAT TGCGCCAATT  
51 CGGTTTCCGC CTGCCATTG ACCCAATCGT TTTCGAGGCT TTGGACTGCC  
101 TTTTGGTCAT CGCCTTCGAC TTGGAACAAT GTTTCAGCA AATCCCGGCA  
151 ACGCGCCACC CATTCTGCAA CCGTCGCAGG TTGCCGCCAT ATCCGTACAA

```

201 TATCCGTCAG GGTTCGAGG AAGCGGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTCTTACC CCACTGCTTC
351 AGGTGAACAG CTGATCCCGT CCGCCGCGCA TTTCTCCGT CAAACCCGAC
401 CGGACGTTCA AATCGCGAAC CGCTCGTGC AAAAGCGGCA AATCGTCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTTCTAAA AGCACAGCA
501 CTTTATCGAC TTCAATCGG CTTTCCAACA AGTCGAACAG GCATAGCAAA
551 GCATGAARCA GCGGTTGTCT GCGGCTGATT TTCACATCCG AAACGGAAAT
601 CGGCAATGCC TGCGCGCCGG GCTGCGCCTG TCCGAACACG TCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

a217.pwp

```

1  VADGVQRQL SGKLRQGFGR LPPDFVFVEA LDCLLVIAFD LEQCQKQIPA
51 TRHPFVNRRL LPYPYNIQR GFEEGGKTSE QGGLVHVIGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFVQ QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRALGLRL SEHGFDKRRR GFDIRG*

```

a217	90.5% identity in 228 aa overlap					
m217.pep	10	20	30	40	50	60
	MADDGVRRQLSGKLRQGFGRLPFDFFVFKVLDXLLVIGFSLEQCFKQIPATRHHPFADRCG					
	:     :     :     :     :     :     :     :					
a217	VADDGVQRQLSGKLRQGFGRLPFDFFVEALDCLLVIAFDLEQCFKQIPATRHHPFVNRRR					
	10	20	30	40	50	60
m217.pep	70	80	90	100	110	120
	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIAAFGOHPAQYHAFYRLLPGEQ					
	:     :     :     :     :     :     :     :					
a217	LPPYPYNIRQGFEEGGKTSEQGGLVHVGI PRADPLPHRIA AFGOHPAQYHAFYRLLPGEQ					
	70	80	90	100	110	120
m217.pep	130	140	150	160	170	180
	LIRAAAHFSVQT PVDVQIGNHHVVQKRXIVLSQSETAQHGRGFXKKHKHPIDFKSAPQQVEQ					
	:     :     :     :     :     :     :     :					
a217	LIRAAAHFSVQTPADVQIGNHHVVQKRQIVLSQSEMAQHGRGFXKKKHPIDFKSAPQQVEQ					
	130	140	150	160	170	180
m217.pep	190	200	210	220		
	AXQSMKQRLA AADFHVXHGI RQCLRTGLRLSEHGFDKKRIGFDIRGX					
	:     :     :     :     :     :     :     :					
a217	AXQSMKQRLS AADFHIRNGI RQCLRAGLRLSEHGFDKKRIGFDIRGX					
	190	200	210	220		

g218.seq

g218.pcp

1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI



502

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGRRPFRAG NRFQRALSVE  
 201 FAQRRGRGMD FVAGFYEL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq  
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG  
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC  
 101 TCGGTGCGGC AGGCGATTAT CTTTGGGAAA CGGCAGCTTC ACTGACCATT  
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGC CGCGCAT  
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAT GGCGCGTTCT TGGTGGCGGA  
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTC  
 301 TGCTGTGCGG GTATTGCTTG GCGGGTATT TGGGCGGCA AGTTCGTACA  
 351 GGCTTGGAGT CAGTTCCTG CCGTAAATG GGTGTGCGAA CCGAACCCCG  
 401 TTTCACTCGT GCCGACCCAC GCGGAGGTAT TGAATGACGG CAAGGTTAAG  
 451 GAAGTGCCGT GGGTTTGGG GCTTACGCCT ATGCTGTGTT CAGGACGAC  
 501 yGtGGGCAAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAACCG  
 551 TCGACCGCTT TCGCGGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA  
 601 TTTGCCCCAA GCGGAGGAC GCGTATGGAC TTTGTGCGAG GATTCTATGA  
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep  
 1 MVAVDPYTAK VVSTMPRNQG WYYTMDIHS DMMLGAAGDY LLETAASLTI  
 51 IMVVSGLYLW WVKRRGIKAM LLPSKXARS WWRNLHGTFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRALSVE  
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMDIHS DMMLGAAGDYLLETAASLTIIMVVSGLYLW					
g218	MVAVDPYTAKVVNTMPRNQGWYHTMDIHS DMMLGAAGDYLLETAASLTIIMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKXARSWWRNLHGTFGTWVSLILLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQRGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVWPVLELTPMPVSGTTVGKDGINPDEPMT					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVWPWILELMPMPVSGTTVGENGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQRALSVEFAQRRGRMDFVAGFYEL					
g218	IGNRRPFRAGNRFQRALSVEFAQRRGRGMDFVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq  
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG  
 51 CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC  
 101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT  
 151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGC CGCGCAT  
 201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GCGCGTTCT TGGTGGCGGA  
 251 ATCTGCACGG CGCGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTT  
 301 TGCCTGTCCG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA  
 351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCGA CCGAACCCCTG  
 401 TTTCAGTCGT GCCGACCCAC GCGAGGTAT TGAATGACGG CAAGGTTAAG  
 451 GAAGTGCCGT GGGTTTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC  
 501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAACCG  
 551 TCGACCGTTT TCGCGG.GA AATCGGTTT AAAGGGCGTT ATCAGCTGAA  
 601 TTTGCCCAAA GCGGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA  
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep  
 1 MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI  
 51 IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLF  
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGE PNPVSVVPTH GEVLNDGKVK  
 151 EVFWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE  
 201 FAQRRGRMD FVAGFYEL

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMD	DEIHS	DMMLGAAGDY	LLETAASLTI	IMVVSGLYLW	
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS	DMMLGSTGDY	LLETAASLTI	IMIISGLYLW		
	10	20	30	40	50	60
m218.pep	WVKRRGIKAMLLPSKXARS	WWRNLHGTFGTWVSLILLF	CLSGIAWAGI	WGGKFVQAWS		
a218	WVKRRGIKAMLLPPKGRARS	WWRNLHGAFGTWVSLILLF	CLSGIAWAGI	WGGKFVQAWS		
	70	80	90	100	110	120
m218.pep	QFPAGKWGE	PNPVSVVPTHGEVLNDGKVK	EVFWVLELTP	MPVSGTTVGK	DGINPDEPMT	
a218	QFPAGKWGE	PNPVSVVPTHGEVLNDGKVK	EVFWVLELTP	MPVSGTTVGK	DGINPDEPMT	
	130	140	150	160	170	180
m218.pep	LETVDRFARX	NRFQRLSAE	FAQRRGRMD	FVAGFYEL		
a218	LETVDRFARX	NRFQRLSAE	FAQRRGRMD	FVAGFYEL		
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1   atgacggcaa ggtaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt gggtagaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaaccgtc gaccgtttcg cgcggaat cggtttcaaa
151 gggcggtatc agttgaattt gcccgaaggc gaggaagggt tatggacttt
201 gtcgcaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatttatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtggt gggaacgctc gtgttctgcc
401 ttgccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaaacgc
451 cgtccgtccg gcgtggcggg cattgttctt ccggcgcaaa aaatcaact
501 gcccgtctgg tggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tcccgaaccg gctgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLAV VFCLAVIFIG ISGCVWWKR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1   ATGACGGCAA GGTTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTCG GCGGnGAAAT CCGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCCGACCGCA
251 CGGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTG GCGGAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATGCGCGCT ATTGGCAATC GCACTGCTCT
551 TCCCCACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1   MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLAV LFCLAVIFIG ISGCVWWKR
151 RPTGAVGIVP PAQKVKLPVW WMMALPLLLI ALLFPTSLLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG					
	:     :     :     :     :					
g219	MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVDRFAREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	:     :     :     :     :					
g219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG					

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
g219	LGWWSVLANVVFCLAVIFIGISGCVMWKRRPSGAVGIVPPAQKIKLPVWAMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1   ATGACGGCAA GGTTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCATATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTGC GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCCGAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CCGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCGG GCGCGGTGGG CATGGTTCCG CCGGCGCAAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCAGCCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1   MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*
  
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
a219	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPSGAVGMVPPAQKIKLPVWAMAVPLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFVKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaatc adatcgacgc tgacggattt gaacctgccc
101 tcacggggcg catcgatgac ttctttggtt tcttcgtagc tttggatgcg
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgctca
201 tgcggttgaa gccgagctcg ccgagcatga ggacgggtgc gcggctgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcgccgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcgccg cggcttttgt ctttggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag gaaagcgggt
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MPADHAEDTF DLFVAQKGRR AAEEVQLGKL VPSVQMWEQ FHFFFKIFDV
151 GIGAAAFVFGD DFVAAAVVAD GVAERNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTGTAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301 ACGTTCGATC TGTTCTGTCG TCAAAAAGGt GCGTGCCCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401 TCTTTTTCAA GATATTGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAIEDH GVAADFARV DGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWE QFHFFFKIFD VGIGAAAFVFG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

m221/g221

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDAVDRRLHFGVE				
	: :                :				
g221	MHDHGAMDRRLPAFGSLMRRVAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR				
	70	80	90	100	110
	120	130	140	150	160
	170				

m221.pep  
CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVK  
|||  
g221  
AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAKRNVNVK  
130 140 150 160 170 180

m221.pep  
GKRFVX  
|||  
g221  
GKRFVX

a221.seq

```
1 ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51 CGACGCTGAC GGATTTGAAC CCGGCTTCGC GCGCGCGATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATCCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTCGATTTCG GCGGGTCGAT TTCGATGGAG
251 TATTCCGCGG TGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTTC
401 ATTTCTTTTT CAAGAAATC GATGTAGGCA TCGCGCGCGG TTTGTCTCC
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGACG
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTA
```

```
a221.pep
  1  MVVLMRLSLV  RQAVNQIDAD  GFEPFRFARRI  DDFGFFVFTL  DAVDRRLHFG
51  VEILNADAVA  VEAESAEHED  GVAADFARVD  FDGVFAGGD*  LEMFAYHAED
101 TFDLVAQAQG  RRAAAEVQLG  KLVPSVQMWS  EQFHFFFKKF  DVGIGAAFVF
151 GDDFVAAAVV  ADGVAERNVN  VKGKRFF*
```

mazz1 95.5% identity in 177 aa overlap

	10	20	30	40	50	60
m221.pep	MXVLMXRSLSVRQAVNQIDAGGFEPFRARRIDDFFGFFVTLD	DAVDRRLHFGVEILNADAHA				
a221	MVVLMLSLSLRQAVNQIDAGGFEPFRARRIDDFFGFFVTLD	DAVDRRLHFGVEILNADAHA				
	10	20	30	40	50	60
	70	80	90	100	110	119
m221.pep	VEAESAEHEDGVAADFARVDFDGVFAGGD	XLEMFAYHAETFDLFVAQKGA-CPAEVQLG				
a221	VEAESAEHEDGVAADFARVDFDGVFAGGD	XLEMFAYHAETFDLVVAQKGRRAAAEVQLG				
	70	80	90	100	110	120
	120	130	140	150	160	170
m221.pep	KLVPVSQVMWSEQHFHFFFKIFDVVGIGAAFVFGDDFVAAAVVADGVAERNVN	VKGKRFVX				
a221	KLVPVSQVMWSEQHFHFFFKIFDVVGIGAAFVFGDDFVAAAVVADGVAERNVN	VKGKRFVX				
	130	140	150	160	170	

g223.seq

```
1 atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51 tttcgatggc gaatttggtct ttgttgcgcg gcgccagttg gaagaattgt
101 tctaaaggca ggttttggct atcgaagccg aaacgggcgg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtta ggagcagctt ggtgtttcca gtttttctcg
251 ccgaggtctt tggcaacgtc gagcagctct gtgtcactga tctctttgcg
301 ccagtatctt tcttgggcga atttcaattc acggaagcgg ccgacacgcg
351 qqaagcctga
```

g223.pcp..

```
m223.seq
1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTGCAAC CATTTGGTCA
51 TTTCGATAGC GAATTGTGCT TTGTACCGC GCGCCAGTTG GAAGAATTGT
101 TCCAAGACAC GGTTTTGCTT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
151 GGTGGCGACT TGCAGGTCGA GGATGTGCTC GTAGAAAGTG AAATCCTAC
201 GGCACGAAA TCGGCGTTGG CAGCGACCTG GTGTTTCCAG TTTCCTCTCG
251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGTGAT TTCTTTGCGC
301 CAGTATTTTT CTTGTGCGAA TTTCAATTGC CGGAAGGCGC CGACACGGCG
351 GAAGCCTGA
```

m223.pep  
1 VEFRHQVVVV GVEFFGHFDS ELVFTARQL EELFQRQVLA VEAEAGGNRA  
51 GGDLDQVEDVV VESEIXYGEN IGVGSDLVFP VFLAQVFSNS QQFLLADFFFA  
101 PVFFLCQEFQF AEGADTREAA\*

```

m223/g223
      10      20      30      40      50      60
m223.pep VEFRHQVVVVGVEPFGHFDSELVFTARQLEELFQRQVLAVEAEAGGNRAGGDQVEDVV
:|||||:|||||:|||||:|||||:|||||:|||||:
g223      MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLAIETGGNRARGYLQVEDVM
      10      20      30      40      50      60
      70      80      90      100     110     120
m223.pep VESEIXYGNIGVGSDDLVPVFLAQVFSNSQQFLADFFAPVFFLCEFFQAEAGDTREAX
:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||:
g223      VESEITYSNVISRSSLVFPVFLAQVFGNVEQLLFTDLFAPVFFLGEFFQETEGADTREAX
      70      80      90      100     110

```

a223.seq

1	GTGGAATTCA	GGCACCAGT	AGTGGTAGTT	GGTGTGCAAC	CATTTGGTCA
51	TTTCGATAGC	GAATTGGTCT	TTGTTACGCG	GCGCCAGTTG	GAAGAATTGT
101	TCCAAGATA	GGTTTTGGCT	GTCGAAGCCG	AAGCGGGCGG	GAATCGCGCC
151	GGTGGCGACT	TGCAGGTCGA	GGATGTGGTC	GTAGAAAGTG	AAATCGCCTA
201	CGGCAACGTA	ATCGGCGTTG	GCAGCGGCGT	GGTGTTTCCA	GTTTTTCTCG
251	CGCAAGTCTT	TAGCAACAGC	CAGCAATTCT	TGCTCGCTGA	TTTCTTTGCG
301	CCAGTATTTT	TCTTGTGCGA	ATTTCAATTC	GCGGAAGGCA	CCGACACGCG
351	GGAAAGCCTGA				

**a223.pep**  
1 VEFRHQVVVV GVEPFGHDFS ELVFTARQL EELFOR\*VLA VEAEAGGNRA  
51 GGDQLQVEDVV VESEIAYGNV IGVSGSLVFP VFLAQVFSNS QQFLADFFA  
101 PVFFLCEQFV AEGTDTREA\*

m223.pep  
 a223

10 20 30 40 50 60  
 VEFRHQVVVVGVPEFGHFDSELVFVTAQRLLELFQRQVLAVEAEAGGNRAGGDLQVEDVV  
 |||||  
 VEFRHQVVVVGVPEFGHFDSELVFVTAQRLLELFQRXVLAVEAEAGGNRAGGDLQVEDVV  
 10 20 30 40 50 60

70 80 90 100 110 120  
 m223.pep  
 a223

VESEIXYGNIEIGVSGDLVFPVFLAQVFSNSQQOFLLDFFAPVFFFLCEQFAEGADTREAX  
 |||||  
 VESEIAYGNVIGVSGSLVFPVFLAQVFSNSQQOFLLDFFAPVFFFLCEQFAEGDTREAX

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1 atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51 tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttaccc
151 gtcaaccgag cccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgcatg gggcttaacg aacagccccgt tgtacgcgtc aaccgagccn
251 ccgccccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatgcgg
301 cttttgggta ttgcctaccg ctacggcgcg acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cagtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tccccgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgccgcg cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgcccgc cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1 MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQVLPV
51 VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKNDPSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1 ..TTTTCAAACC CGGCAGTTTG GCGGTTTTTG TGGCTGAWGT TTGCCGTCCG
51 CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTTTACC CATCAACCGA
151 GCCCCGCCCC GCGGCGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCC TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCGTCAA CCGAGCCCCC GCCCGGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGGCGGCAC ATCGGTTTCT ACCGGTTTTG ACTGCAGCGG CTTTCATGCAG
451 CACATCTTCA AACCGCCCAT GGGCATCAAC CTGCCCGGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551 ATATGGTGT TTTCCGACG CTCGCGGCA GCGCATTC CATGTCCGA
601 CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCCGCCG GGTCAAGAAA AACGACCCGT CCCGCTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1 ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51 APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QPVLVNRAP ARRAGNADEL IGNAMLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRISHVG
201 LYIGNNRFIH APRTGKNI EI TSLSHKYWSG KYAFARRVVK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

```

          10      20      30      40      50
m225.pep  FSNPAVWAVLWLXFAVRPALADELTNLSSREQILRQFAEDEQVLPINRAPARRAG
          | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g225      MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQVLPVNRAPARRAG
```



510

	10	20	30	40	50	60
	60	70	80	90	100	110
m225.pep	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
	:       :					
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA					
				70	80	90
	120	130	140	150	160	170
m225.pep	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
	:     :					
g225	DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
	180	190	200	210	220	230
m225.pep	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIETSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIETSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
	240	249				
m225.pep	VKKNDSRFLNX					
g225	VKKNDSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGGC GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCCGTTT ACCCGTCAAC CGAGTCCCGC CCGGCGGGG
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTTCG
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG				
	:				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225.pep	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				

511

```

      |||
a225  NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
      70      80      90      100      110      120

      90      100      110      120      130      140
m225.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      |||
a225  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      130      140      150      160      170      180

      150      160      170      180      190      200
m225.pep MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      |||
a225  MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVFXFRTLGGSRISHVGLYIGNNRF
      190      200      210      220      230      240

      210      220      230      240      249
m225.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDRPSRFLNX
      |||
a225  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDRPSRFLNX
      250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

```

g225-1.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttaccc
151  gtcaaccgag ccccccgcgc gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggccttaacg aacagcccg tgtacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcacggcgag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcgcg acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgcgcgc cagtcgcggc gaacaggcgc gcatggcgcg acccgttgcc
451  cgaagcgcaat tgcagcccgg ggatatgggt tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtgc gactttatat cggcaacaac cgcttcatcc
551  acgcccgcgc cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gtccgcccgc cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

```

g225-1.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FADEQPVLP
51  VNRAFPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDRSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

```

m225-1.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGTG GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTGCCCgaag ACGAACAGCC CGTTTACCC
151  ATCAACCGAG CCCCCGCCCC GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CCGATGGGG
301  CTTAACGAAC AGCCCGTTT ACCCGTCAAC CGAGCCCCCG CCGGCGGGC
351  GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGTG TTCCGCACGC TCGGCGGCAG CCGCATTTC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCAGC CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGAGCGGCA
701  AATACGCGTT CGCCCGCCGG GTCAAGAAAA ACGACCCGTC CCGCTTCTG
751  AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IETSLSHKY WSGKYAFARR VKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep  MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
              |||:|||||
g225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPVNRAPARRAG
              10      20      30      40      50      60

              70      80      90      100     110     120
m225-1.pep  NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
              |||
g225-1      NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
              70      80      90

              130     140     150     160     170     180
m225-1.pep  DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
              |||:|||||
g225-1      DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep  SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
              |||:|||||
g225-1      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep  VKKNDPSRFLNX
              |||:|||||
g225-1      VKKNDPSRFLNX
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTGCGCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC GCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGGCGGG CAATGCCGAC
451 GAACATCATG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CCGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTCCCAT GTCCGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCCA GCCTGAGCCA CAAATATTGG AGCGGCAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDPSRFLN *

```

a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
            |||||
m225-1     MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
            |||||
      10      20      30      40      50      60

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
            |||||
m225-1     NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA
            |||||
      70      80      90

      130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
            |||||
m225-1     DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
            |||||
      100     110     120     130     140     150

      190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
            |||||
m225-1     MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
            |||||
      160     170     180     190     200     210

      250     260     270     280
a225-1.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKQNDPSRFLNX
            |||||
m225-1     IHAPRTGKNIEITSLSHKYWSGKYAFARRVKQNDPSRFLNX
            |||||
      220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

```

g226.seq
1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTCGCGATTA TCGTGCACAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGcATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcc
451 tttctgttgc ctccgcctct cctgcgcgcg ctcggcccg atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggc ctttctcct Cggggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

```

g226.pep
1  MSEILRQPSV LLFLTLAVYA LAIVRTRTG NIFCNPVLS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
101 GSVTGIVTGM YFAAWLGPDT QSFPPRLQY LLFTPSGIPI HTLYARVLP
151 FLLPPLPR LGPHTLRRFT ILPKLRPFK PLLPVVLSL PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

```

m226.seq
1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTCGCGATTA TCGTGCACAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGCATTGT TACAGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGTTACAA

```

514

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTTGGT ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TCATCCCGT TTTGGGATT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep  
 1 MNEILRQPSV LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNI FCNPVLVSTIVLIAYLKILGIDYAVYHN					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNI FCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
g226	QFSFPRLQYLLFTPSGIPHTLYARVLPPFLPPPLPRLGPHTLRRFTILPKKLRPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq  
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC  
 51 CGGTACGCG CTTCGATTA TCGTGCAC GCGCAGGGT AATATCTTCT  
 101 GCAACCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC  
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATT  
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC  
 251 GCCGTAAAT CTTCACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGGC  
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG  
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC  
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC  
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA  
 501 AATGTTGAAA AACACGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TTATCCCGT TTTGGGATT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep  
 1 MNEILRQPSI LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep      MNEILRQPSVLLFLTAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
a226          |||||:|||||
              10      20      30      40      50      60

              70      80      90      100     110     120
m226.pep      AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAE
a226          |||||:|||||
              70      80      90      100     110     120

              130     140     150     160     170     180
m226.pep      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPS
a226          |||||:|||||
              130     140     150     160     170     180

              190     200     210     220     230
m226.pep      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
a226          |||||:|||||
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcgctgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccggc agcatcgctc
101 gcatggcgct gctgtttgct cttttgcagg cgggttggt caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttctc
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLEP SIVGMGVLEA LLQAGWLKTS
51  WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTkgc TGCAACAGCT TACCGACGCG CTGATGTGCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTG GATTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

m227/g227

```

m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
g227          TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
              20      30      40      50      60      70

              40      50      60

```

516

```

m227.pep    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
             |||||||||||||||||||||||||||||:||||
g227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
             80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1   ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51  CGAAACCGCC GTTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTGC
101 GCATGGGCGT ACTGTTTGCG CTTTTCGAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TGGCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGTTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1   MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LQAGWVKTS
51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep                                10      20      30
                                TSXLQQLTDALMSNLTFLVPPCVAVISYL
                                || |||||||||:|||||||||||||||
a227      TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
           20      30      40      50      60      70

           40      50      60
m227.pep    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
             |||||||||||||||||||||||||||||:||||
a227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
             80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1   ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCCGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1   MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLTK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1   ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCCGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

```

a228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

m228/a228 100.0% identity in 107 aa overlap

```

          10      20      30      40      50      60
m228.pep  MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
          |||
a228       MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
          10      20      30      40      50      60

          70      80      90      100
m228.pep  AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
          |||
a228       AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
          70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

```

g229.seq
1  atggctgccg tatcgggcgg cggtgcggtc ttcctgataa tgcttcaca
51  tattgcccg cgttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtgc cgcccaagag
151 gttttgccc acaaacggca cggtgccgaa cgagcggtt accgaacggt
201 tttgatggcc gaacgacagg cgcaggttct gttcgctgaa atctttgta
251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgcc
301 gcccgattg atttcgcgcg acacgcccaa gccgtagcgc aaaccgtgtg
351 ccttttgccg caggtgtcgc gcggttttcg tccagcttct gcccgcaaat
401 tcaatcgttt ttccggacga agcgtgtgtt atagcggatt acaaaaaatc
451 aggacaaggc ggcgggccgc aggcagtacg gatggtacgg aaccggttcg
501 cccggtgctt ggacgcctta gggaaccgtt ccttttgagc cggggcgggg
551 caaccgtac cggtttttgt tcatccgcca tattgtgttg a

```

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

```

g229.pep
1  MAAVSGGGAV FLIMLPHIAR VOROPPAFAQ ASGEIGIEAA GEIVSAAAOE
51  VLPDKRHGAE RARYRTVLMA ERQAQVLF AE IFVIPIMHAA ADAAVEEMMP
101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRF FGR SVVYSGLT KI
151 RTRRRAAGST DGETPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

```

m229.seq (partial)
1  ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
51  GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTGCGCGCA CACGCCTAAG
251 CCCTAGCGCA AACCGTGTGC CTTTGCGGC AGGCTGTCGG CGGTTTTTCGT
301 CCAGCTTCTG CCCGCAAAAT CAATCGTTTT TTCGGACGAA GCGTTGTTTA
351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
401 AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACCTTA GAGAATCGTT
451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

```

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

```

m229.pep (partial)
1  ..AQALGEIGIE ADEIVSAAA KEVLLDKRHD AERARYRTVF IAERQAQALF
51  AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTV LRLQAVGGFR
101 PASARKFNRF FGRSVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
151 SLFCSSAILC *

```

Computer analysis of this amino acid sequence gave the following results:



# Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      MAVVSGGGAVFLITLPHIAHVQRQPPAFQAASGEIGIEAADEIVSAAAXEVLPDKRHGAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RARYRTVLMARQAQVLF AEIVFVIMHAAA-DA AVEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRQRSADSTNSTEPIHLVLQHLRE----
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRRRRAGSTDGTEPVRPVLGRRLREPFFL
                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSLFCSSAILCX
                :|: ||| ||| |||
g229      SRGGATRGTGFCSSAILC
                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

```

a229.seq (partial)
1  ATGGCTGTCG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51  TATTGCCAC  GTTCAGCGTC AGCCGCCA. . GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTGTCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAAATGATG
301 CCGGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTCAATCG TTTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTACGACC TTAGAGAATC GTCTCTTTGA GCTAAGGCGA
551 GGCAACGCCG TACTGGTTTT TGTTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

```

a229.pep (partial)
1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51  VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTG
151 ITRRRRSADS TDSTEPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFVIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      XARYXTVFIAERQAQALFAEIVFVILIVHAAAADVSEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110     120

```

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	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
	:     :     :     :     :     :					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
	:     :					
a229	AKARQRRTGFCSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttccatt ccacgaaaa atacagaaca cccgccaag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gttcccatc
101 cgggcgccga ctacatcgtc caagtggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgcatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaacacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtgtg
401 tcgaagaaat ccgcgatcag tttgccttgc agaatttggg aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcacgcccc agtcaaagcg tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaatatgt
651 cgcccttgaa ctgaaggatt ttgcagacaa gcagaccgtc agtgaacagg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaaaga aagctgggag
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaacacca agaaacttgg ctgagcagggc aggacgcaca
951 aatgtccggc atgcccgaag acctaataca tgcggtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tgcgtcaggg ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEIQKM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKPYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEK A VENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKNLLFEEA KDAVRQAYIR TEAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GcC.GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCTTGC AGAATTGGT AAACCTCGTC

```

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```

451 CAAACGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTGCGAA ACGAATTGAA
801 AATGAAAAAG GCGGTGCGCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPDA VFQSLQRAY LKQGAKLMI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKQFN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKK AVADFNKAKE KLGDVAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLITINSET
351 AWVVRKEVR EEKTLPPAEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPDAVFQSLQRAYLKQGAKLMI SVSSEIQKIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAKLMI SVSSEIQKMIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m230.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m230.pep	PDEFIAQVKVSEADLQKFYNANKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m230.pep	ERVARLPANEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
g230	ERVARLPANEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRakeVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRakeVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCAACGTCAT TATGTCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGACGGTC AACCACACCA TCCGTTTCGA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAGAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAAGTC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVSTV SHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAALMI SVSSEIQIKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHNSVLTINSET
351 AWVVRakeVR EEKTLPF AEAKDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPSDAVFQSLQRAYLKQGAALMISVSSEIQIKIIVDDPNFHDANGKFDHALLN					
a230	ADGGGPSDAVFQSLQRAYLKQGAALMISVSSEIQIKIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

```

m230.pep  RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN
          130      140      150      160      170      180

          190      200      210      220      230      240
m230.pep  PDEFIAQVKVSEADLQKFYNANKKDYLKPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      PDEFIAQVKVSEADLQKFYNANKKDYLKPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          190      200      210      220      230      240

          250      260      270      280      290      300
m230.pep  ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
          250      260      270      280      290      300

          310      320      330      340      350      360
m230.pep  GLKVVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a230      GLKVVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR
          310      320      330      340      350      360

          370      380
m230.pep  EEKTLPF AEAKDAVRQAYIRTEAAKL
          ||||||||||||||||||||||||||||||||||
a230      EEKTLPF AEAKDAVRQAYIRTEAAKL
          370      380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

```

g230-1.seq
1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCTATC
101 CGGCGCCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCACTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCCTTG AGAATTTGGT AAGCCTCGTC
451 CAAACCGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTTC AAC CCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAAT TGGAATATGT
651 CGCCTTGAA CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGGCTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGA AAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATCGGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCGAAA ACCTAATCAA TGCCGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGCTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCTGCGA AACAGGCTTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTTCA CCTGCTGATC CGCTATTCA ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

```

g230-1.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGA LMG I SVSSEIQKQM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHMSDQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRakeVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPPPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNGD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACCGG GTGTTCCAAT CCTGCTGCA ACGCGCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAAAT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCCG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTGGC GGCAATGAA
751 GCGCAACCTT CTTTCGAGCA GGAAAAAGCC GCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GCGTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGAGC
1001 TATTGAAGAA AAAACACAA TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCGCTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAAACAG GCAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCGAGGCG TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTGCAAGT ACAGGCTGTA ACCCGCGCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTGTGTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGA KLMI SVSSEIQIKI
101 IVDNPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRakeVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAR QSMPPPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPEDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNGD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDH	SINNAIQNEQ				
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGA KLMI SVSSEIQIKI	IVDDPNFHDANGKFDHALLN				
g230-1	ADGGSPWRDAVFQSLQRAYLKQGA KLMI SVSSEIQIKMI	VDNPNFHDANGKFSHALLS				
	70	80	90	100	110	120
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGA KLMI SVSSEIQIKI	IVDDPNFHDANGKFDHALLN				
g230-1	ADGGSPWRDAVFQSLQRAYLKQGA KLMI SVSSEIQIKMI	VDNPNFHDANGKFSHALLS				
	130	140	150	160	170	180
m230-1.pep	RYLSQRHME	DQFVEEIRDQ	FALQNLVNLV	QNGVLVGDAQAEQLIRLTQV	NRTIRSHTFN	

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```

g230-1      :|||||:|||||:|||||:|||||:|||||:
              QYLSQRHMSDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLRLTQVNRRTIRSHTFN
              130      140      150      160      170      180

m230-1.pep  190      200      210      220      230      240
              PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
              |||||:|||||:|||||:|||||:|||||:
g230-1      190      200      210      220      230      240
              PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
              |||||:|||||:|||||:|||||:|||||:

m230-1.pep  250      260      270      280      290      300
              ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
              |||||:|||||:|||||:|||||:|||||:
g230-1      250      260      270      280      290      300
              ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
              |||||:|||||:|||||:|||||:|||||:

m230-1.pep  310      320      330      340      350      360
              GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNEVLITINSETAWVVRKEVR
              |||||:|||||:|||||:|||||:|||||:
g230-1      310      320      330      340      350      360
              GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNEVLITINSETAWVVRKEVR
              |||||:|||||:|||||:|||||:|||||:

m230-1.pep  370      380      390      400      410      420
              EEKTLPF AEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR
              |||||:|||||:|||||:|||||:|||||:
g230-1      370      380      390      400      410      420
              EEKNLLFEEAKDAVRQAYIRTEAAKLAENKAKEVLTLQNGGKAVDVKWSEVSVLGAQQAR
              |||||:|||||:|||||:|||||:|||||:

m230-1.pep  430      440      450      460      470      480
              QSMPP EAYAE LLKAKPANGKPAYVRLTGLPAPVIVEQAVTPPDDIAAQLPLAKQALAAQ
              |||||:|||||:|||||:|||||:|||||:
g230-1      430      440      450      460      470      480
              QSMPP EAYAE LLKAKPANGKPAYVRLTGLPAPVIVEQAVTPPEDIAAQLPPAKQALAAQ
              |||||:|||||:|||||:|||||:|||||:

m230-1.pep  490      500      510
              QSANTFDLLIRYFNGKIKQTKGAQSV DNGDGQX
              |||||:|||||:|||||:
g230-1      490      500      510
              QSANTFDLLIRYFNGKIKQTKGAQSV DNGDGQX
              |||||:|||||:|||||:

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 837>:

```

a230-1.seq
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCGAAT CCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTGCGCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAAACAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAAATATG
651 CGCCTTGAA TCGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGA AAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTGCGG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCGAAA ACCTGATCAA TGCGGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTG TCCGCGCCAA AGAAGTCCCG GAAGAGAAAA CCTGCGCTT
1101 TGCCGAAGCC AAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAAACA GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGCG AAACGGCAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCGCCCG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTGTTTGATA CGTTATTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGCGGAC GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

## a230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFGVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKTLPFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAQ QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

## a230-1/m230-1 99.8% identity in 512 aa overlap

	10	20	30	40	50	60
a230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
m230-1	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
m230-1	ADGGGSPSRDAVFQSLQRAYLKQGAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a230-1.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
m230-1	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a230-1.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
m230-1	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a230-1.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
m230-1	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300
	310	320	330	340	350	360
a230-1.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
m230-1	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380	390	400	410	420
a230-1.pep	EEKTLPFAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVWKSEVSVLGAQQAQ					
m230-1	EEKTLPFAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVWKSEVSVLGAQQAQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
a230-1.pep	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPPDDIAAQLPLAKQALAAQ					
m230-1	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPPDDIAAQLPLAKQALAAQ					
	430	440	450	460	470	480
	490	500	510			
a230-1.pep	QSANTFDLLIRYFNGKIKQTKGAQSVNDGDGQX					
m230-1	QSANTFDLLIRYFNGKIKQTKGAQSVNDGDGQX					
	490	500	510			



This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTGCGCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTG GTGTGGAACA
501 CCGGACGCT GACTTTCCTG CCTCCGCGC CCGCGCGCAG GTTGTGCGGC
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCTGTGT AGCGGTGCGC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFFP RLNLVGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFPG					
a231	QSRVSLPNAQPFAGHIHPI LIAPAAPACPAVRPRRLRIFSFPQSFAFFPRLNLVGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTGCGCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTG GTTTCAAACa
501 CaCgTaCaat gagtttcgtA ccctccGCCG ccgcgcgCAG GTTGTcgcGC
551 GAACgTGTAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGTttcgcgc cgtcgcCgtc gATGACGTGA AGGGtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGAttctgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51 ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFPQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF  
 151 AGGYLRHFAL IAVGFKHTYN EFTRLRRRAQ VVARTCTVSV FHLRCVDIRH  
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq  
 1 ATGTCAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC  
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCTGA  
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG  
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT  
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC  
 251 CCGCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT  
 301 AGCTTTCCAC AATCCTTTC GTTCCCTTC CGCTGAATT TGAGCGTCGG  
 351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA  
 401 TAATGCCACG CGGCCCGTC CTGCACTGCA ATCAGGTTCA AATCGGTTT  
 451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTG GTATCGAACA  
 501 CGCGCAGGCT GACTTTCCTG CCTCCGCGG CGCGCGCGAG GTTGTCGCGC  
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT  
 601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGCTGTCGC  
 651 CGTCATAGAC TTTGGACACC GTGCTGTGT AGCGGTGGCC GGATTTCGCC  
 701 GATGCTCGGC GCGGGCGGG CGCGTCGGA CCCGCGTCCC CTGCCGCGCC  
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC  
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC  
 851 ATGATTTTTT TAATCTGCAT ATTTTCAA TGCCGATGCC GTCTGAACAT  
 901 ATCGGAATCG GATTTCAGAC GGCATCTTA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep  
 1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR  
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF  
 101 SFPQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF  
 151 ADRNLRHFAL VAVGIEHAHA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH  
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA  
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH  
 301 IGIGFQTAS\*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFRLNLVGIIVG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFQSFAPFRLNLVGIIVG					
	70	80	90	100	110	120
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFRLNLVGIIVG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFQSFAPFRLNLVGIIVG					
	70	80	90	100	110	120
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFTRLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRNLRFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFTRLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRNLRFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHFNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCASAGG					
	190	200	210	220	230	240
g231-1.pep	VVARTCTVSVFHLRCVDIRHFNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCASAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVGXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq  
 1 ATGTCAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC  
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCTGA  
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCG TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCGCTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTCGAACA
501 CCGGAGCGCT GACTTTCCTG CCTTCCGCGC CCGCGCGCAG GTTGTGCGGC
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGTTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTGCGC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGCTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

```

a231-1.pep
  1 MSKRKSINRP YOKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFQSFAPFP RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFV				
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFV				
	70	80	90	100	110	120
a231-1.pep	QSRVSLPNAQPF	FAHGIHPILIAPAACP	PAVRPRLRIFS	SFQSFAPF	RLNLVGIIG	
m231-1	QSRVSLPNAQPF	FAHGIHPILIAPAACP	SAVRPRLRIFS	SFQSFAPF	RLNLVGIIG	
	130	140	150	160	170	180
a231-1.pep	KIRLILFFSIT	TFIMPRRPV	LHLHQVQIGF	ADRNLRFH	FALVAVGVEHAD	DFPAFRRAQ
m231-1	KIRLILFFSIT	TFIMPRRPV	LHLHQVQIGF	ADRNLRFH	FALVAVGVEHAD	DFPAFRRAQ
	190	200	210	220	230	240
a231-1.pep	VVARTRAVSLF	HLLRRVDIRH	PDFVFRVAV	DNVKGVAVID	FGHRACVAV	GFRRCSAAGG
m231-1	VVARTRAVSLF	HLLRRVDIRH	PDFVFRVAV	DNVKGVAVID	FGHRACVAV	GFRRCSAAGG
	250	260	270	280	290	300
a231-1.pep	RVGTRVPCRAEY	VEYGNRRP	HRLAAVPRIT	QRTQKRQGDG	KPFHDFNLH	IFQMPMPSEH
m231-1	RVGTRVPCRAEY	VEYGNRRP	HRLAAVPRIT	QRTQKRQGDG	KPFHDFNLH	IFQMPMPSEH
	310					
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

```

g232.seq
  1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatcctggt
 51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt ttgtctggtc gccgtcggag gaacggccgg cagcctggtt

```

530

```

151 atgccgtccg tacccgccaa ggctgccgat acccaaatcg agtggaaatat
201 tgtcccggtg acaaaatccc tgctgcgtga aacgggtcgg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg cgggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgcccgcg
401 gttcggtagt gtgtgccaaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacgggt tcgggcctgg ttttggtgtg
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggatgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttcgctc tatacctggc tgcaaacgcg
651 cagcagcgag acttttcggc cccgcgcgtg tgcgcgcaac aatatcgta
701 acggcatctt tatggtttcc gccgcggtt tgagcgcggt attgctgttt
751 ttggttgaca gcatttccct gctgtatctg attgtcgcct tgggcaatat
801 tccgttgggc gtatttttga ttaagcgcga aaggcgggtt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRRTVR HNPVFTAIIG ISWFWFGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRRERF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51 CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTGGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC ACAAATCCC TGCTGCGTGA AACGGTGGCG CACAAGCCCG
251 TTTTACCAGC CATTATCGGT ATTTCTGGT TTTGGTTGT CCGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTGACGGTT TCGCGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTTCTC CGTTCGCTC TATACCT (g) TG CAAACCGCCA
651 TAGCGAGATT TCCGCGCCCG GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGTT TTTCCGCTGC CGTTTGTGAG CCGGTGTTGC TGTTTGTGTT
751 TGACAGCATT TCCTTGTTGT ATCTGATTGT CGCTTTGGGC AATATCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRRTVR HKPVFTAIIG ISWFWFGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERREFG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

          10      20      30      40      50      60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||||:|||||:|||||:|||||:|||||:|||||
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
m232 . pep	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPFVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	70	80	90	100	110	120
m232 . pep	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	130	140	150	160	170	180
m232 . pep	190	200	210	220	230	
	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
	190	200	210	220	230	240
m232 . pep	240	250	260	270	280	289
	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232 . seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTC
101 AAACCGCGCT GTTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAACATG GCGCGTTCG TGTATTATTT
201 GCCGTATTTC CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCCGC TGCTTTTGGC
351 GTGCTCTGTT TGCATGGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGTAC GTTTGTCGCC ATCCTGTTTC GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGTTT
551 TGCTGGTCGC CGTAGGAGG ACGGTCGGCA GCCTGTTTAT GCCGTCGGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTG GCGCGGTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGAA CGGCTGAGT TGGCTTGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTT CGGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTCGGCGGA
1051 TTTTCTCCG TTCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACA TATCGTTAAC GGTATTTT
1151 TGGTTTCCGC TGCCGTTTGT AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTATT AAGCGCGAAA GGCGTTTTT AGGCGCGCG GCAATCAGGA
1301 AAAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232 . pep
1  MYAKKGGGLGL VKSRFPAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFFVA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNML ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

532

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG  
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS  
 401 ISLLYLIVLAL GNIPLSVFLI KRERREFLGAA AIRKKP\*

m232/a232 95.9% identity in 290 aa overlap

					10	20	30
m232.pep					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLCMGAQSTLFGPLKYAILPDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP						
	120	130	140	150	160	170	
	40	50	60	70	80	90	
m232.pep	YIVGILVLLVAVGGTVGSLEMPSPVAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG						
a232	YIVGILVLLVAVGGTVGSLEMPSPVAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG						
	180	190	200	210	220	230	
	100	110	120	130	140	150	
m232.pep	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSXERLMLAW						
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSRERLRLAW						
	240	250	260	270	280	290	
	160	170	180	190	200	210	
m232.pep	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL						
a232	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL						
	300	310	320	330	340	350	
	220	230	240	250	260		
m232.pep	YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVLALGNIPLS						
	:    ::						
a232	YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVLALGNIPLS						
	360	370	380	390	400	410	
	270	280	289				
m232.pep	VFLIKRERREFLGAAAIRKKPX						
a232	VFLIKRERREFLGAAAIRKKPX						
	420	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq  
 1 atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtcgc  
 51 ttccggtgcg gacaaaccca agcaatatgt cgaaatcgga agcaaaaccg  
 101 ttttagaaca tgtacttggg attttgaac ggcatgaggc cgtcgatttg  
 151 accgtcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac  
 201 ggcatttcca caggttcggg tgtggaaaaa cggaggacag acccgcgccg  
 251 aaactgtccg caacggtgtg gcaaaactgt tggaaaccgg tttggcggcg  
 301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc  
 351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg  
 401 ggattttggc agttcccgtt gccgatacgc tcaagcgcgc agaaagcgga  
 451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgcaaacgcc  
 501 gcagcttttt caagcgggtt tgctgcaccg cgcatgtgct gcggaaaact  
 551 tgggcggcat taccgatgaa gcgtccgccc tggaaaaact ggggtgtcgt  
 601 ccgctactga tacagggcga cgcgcgcaat ttgaaactga cgcagccgca  
 651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga

This corresponds to the amino acid sequence &lt;SEQ ID 858; ORF 233.ng&gt;:

g233.pep  
 1 MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNGGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNILVHDA ARCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR  
 201 PLLIQGDARN LKLTQPDAY IVRLLLNAV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCGA CAGGTTCCGG TGTGGAAGAA CGGCGGACAG ACCCGCGCCG  
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGCGC  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG  
 401 GGATTTTGGC AATTCCCATT GCCGATACGC TCAAGTGC GCACGGTGGG  
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)  
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG  
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq  
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCGA CAGGTTCCGG TGTGGAAGAA CGGCGGACAG ACCCGCGCCG  
 251 AAACGTGTCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG  
 401 GGATTTTGGC AATTCCCATT GCCGATACGC TCAAGTGC GCACGGTGGG  
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC  
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAACT  
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCCG  
 601 CCTTGCTGGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA  
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA



This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGAREFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

      10      20      30      40      50      60
m233.pep  MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          |||
a233      MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          10      20      30      40      50      60

      70      80      90     100     110     120
m233.pep  FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          |||
a233      FADKVQTAFPQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          70      80      90     100     110     120

      130     140     150
m233.pep  TRLIEQAGNA AEGGILAIPIADTLKCADGGNI
          |||
a233      TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
          130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPQDAYIVRLLLDVAVX
          190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat caccgtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgtccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttccgg caaagcgag aacctgaaag gcgagatta
351 tgcgttacc ggcgatgtaa cgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcgga aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agtttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATSSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRNFV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGTSGY DATLNGKVL D
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTGA GACTTGGCAA
101 TCCGCGAAGC .GTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

m234.pep (partial)  
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW  
 51 QPNR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng)  
 from *N. gonorrhoeae*:

m234/g234

						10	20	30
m234.pep						GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL				
	140	150	160	170	180	190		

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
	:		
g234	DLAIREAVDNLVQAVDNGAWQSNRX		
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)  
 1 AACCGCACCT ATTTGAACGC ATTAAAACAG GAATCCGGCA TTTCCGGCAA  
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG  
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT  
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA  
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG  
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT  
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA  
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)  
 1 NRTYLNALKQ ESGISGAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG  
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD  
 101 ATLNGKVLDL AIREAVNSLV QAVDNGAWQP NR\*

m234/a234 100.0% identity in 54 aa overlap

						10	20
30							
m234.pep						GAGEYALSNREI	IGFGGTSGY
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL			
	50	60	70	80	90	100	

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
a234	DLAIREAVNSLVQAVDNGAWQPNRX		
	110	120	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

536

```

1  atgaaacctt tgatttttagg gcttgccgcc gtgttggttc tgtctgcctg
51  ccaagttcga aaagctcccc acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aattttggtg gttccgccgc tgaacgagtc gcctgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga tttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggctggt cgattcccg caggggaaag agttgtggtc ggggtcggcc
451 agcatccgca aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgccaa cagcctgacc gaccgcggtt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattcccg
601 aacggtatct tgaagggtcc gagattcgtc gaagagcagc ccaataaa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCG CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTACAG CCGTCCGGCC GGAAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTGT TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCTGT TGGGGGCTTT
501 GGTACGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQENGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng)

from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQENGLTNAADIHAVRPEKLHQIFGNDAVLITVTEYGTS					
g235	AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
g235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCTGACTA CACGTCATT C AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TGCGGTTTGG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||
          10      20      30      40      50      60

          70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||
          70      80      90      100     110     120

          130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
          130     140     150     160     170     180

          190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTG ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCGGCGGC GGTAATTTCTG
251 GCTTCCGCTT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAgTTC GGCTTCGGCT TTTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGGGCGGGC GCGGCTGTCTG
551 GCTTTGTGTG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTGAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCTT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacag AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGGCCGTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TGC GCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGGNGKFI
51 TDFHFCFRHQ QGKAQFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV PHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAO
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATG CCGTCCATTT TTTCACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCTCTTCGC CGCCGCCGwT GayGTCCAC GCTTCTTCG
201 CGGTGAAGCA CAAATCGGT GCAATCAAGA GAACCAACT GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACAATG TCTTTACGG CAAAGTGGAa kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GCGGTAGCGG TCGATTTCCTA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPME
51 EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQGS LC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXFYQKVE XITRIVIACQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQO
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng)

from *N. gonorrhoeae*:

m236/g236

539

					10	20	30
m236.pep					LHGR	TDGFVGAQRLDGGGYRFAGFADCRPF	
g236	FRHQQGKAQFFAQSIQIAGHFFRRGNFGFRLQGR	TDSFVGAQRLDGGGYCFARFADCRPF					
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
	FHQFGFGFFVDGREL	VPSMEEDAVXFAAAXD	VPFRFFAGEAQNRCNQENQ	TACDVIQGS	LC		
g236	FHQFGFGFFVDGREL	VPSMEEDAVF	FAAADDPFRFFAGEAQNRCNQENQAARDV	VQGGLR			
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
	AAACMAVCFGGVEAVFQDVE	VERTQVFRAERNXV	FYGVK	VE	ITRIV	IACQTL	LQLTCQYH
g236	AAAGAAVGGFVGVEAVFQDVE	VERAQVFRAERNNV	FHGEVEGI	ARIVTACQ	TLLQPP	RQYQ	
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
	GVAVDFHHIRLLHGIFNRIK	VAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGR	CR				
g236	GVAVDFHHIRLLHGIFNRIK	VAQIGKQEAQGIADA	AAVAFGNAFEDFFGNRQFAAVIGGCR				
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
	PQAQDVCAEFVINLLRCNDVADGFRHFAFAVDNETMGQQLFIR	RATHX					
g236	PQAQDVRAEFVIDFLRRDDVADGFRHFAAVLVNHETVGQQLFIR	CASHG					
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCAGA
51  CGGTTTCATG GCCTGCAACC GCGCCACAT CCGGGGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTCACCATC ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCCTACTTTC ACTTCTGCTT TAGACACCAG CAAAGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCGCGCGC GGTAATTTTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTGCGGCG GCAAAGGCTC
301 GATGGCGGCG GTTACCGCTT CGCGGGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAAGTC GGCTTCGGCT TTTTCGTTGA TGGTCGGGAA CTCGTGCCAA
401 GTATGGAAA GCACGCTGTC TTCTGCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCGG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGGCG TCGGCGGGC GCGGCTGTCTG
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTT TTTACCGCA AAGTGGGAAGG
651 CATAACGCGG ATAAAAATCA CCGGCAACGC GTTCTTGCA CCGCCTTGCC
701 AACACCAAGG CATAGCGGTC GATTTCACC ATATCCGCCT GTTGACGGC
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGA GATTTCCTTG
851 GAAATCGCCA ATTCGCGGCT GTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCGCG CCGAACTCGT TATACACTTC TTGCGGCGC ACGACGTTGC
951 CGATGGATT CGACATTTT CGCCCGTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTGTACGG CGCGGACCC ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```

a236.pep
1  MARFAFSADI LCTAFADGFM ACNRAHIAGV VPAAFAFFTI TGFSGNGKFA
51  AYPHF CFRHQ QSKAQFFAQS IQIAGHFFRR GNFGFGLQGR TDGFVGAQRL
101 DGGGYRFAGF ADCRPFHQF GFGFFVDGRE LVPSMEKHAV FCAAADDVPR
151 FFAGEAQNRC NQENQAARDV VQGGLRAAAG AAVGFGGIEA VFQDIEVERA
201 QVFRAERNHF FHGKVEGTR IKITGNAFLQ PPCQHOGIAV DFHHIRLLHG
251 IFNRIEVAQV GKQKAQGIAD TAVAFGYALE DFFGNRQFAA VIGGCRPQQAQ
301 DVRAELVIHF LRRDDVADGF RHFAPVLIHH ETMGQQLFVR RATH*

```

540

m236/a236 81.0% identity in 258 aa overlap

m236.pep					10	20	30
					LHGRTDGFVGAQRLDGGGYRFAGFADCRPF		
a236	FRHQQSKAQFFAQSIQIAGHFFRRGNFGFLQGR	TDGFVGAQRLDGGGYRFAGFADCRPF					
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
		FHQFGFGFFVDGRELVP	SMEE	DAVXFAA	XDVP	PRFFAGEAQNRCNQENQTACDV	IQGSLC
a236		FHQFGFGFFVDGRELVP	SMKHAVFCAA	ADDVPRFFAGEAQNRCNQENQAARDV	VQGG	LR	
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
		AAACMAVCFG	VEAVFQD	VEVERTQVFRAERNXVFY	GKVEXITRIVIA	CQTLLQ	LTCCQYH
a236		AAAGAAVGF	GIEAVFQDIE	VERAQVFRAERNHFFHGK	VEGITRIKITGNA	FLQPPC	QH
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
		GVAVD	FHHIRLLHGI	FNRIKVAQVGKQKAQGI	ADTAVAFGYAFEDFFGN	RQFAAV	IGRCR
a236		GIAVD	FHHIRLLHGI	FNRIEVAQVGKQKAQGI	ADTAVAFGYALEFFGN	RQFAAV	IGGCR
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
		PQAQDVCAEFVINLLRCND	VADGFRHFFAFVDNETM	GQQLFIR	RATHX		
a236		PQAQDVRAELVIHFLRRDD	VADGFRHFAPVLIH	HETMGQQLFVR	RATHX		
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq

```

1  atgcgggaca aggttggcgg taatatcgca ctccccgccc cacgaatatt
51  cgattctaac atcggaagc tgcggaaaaa ctttaagcat atcttgccgg
101 acaagctcgg tcatacgcg aggattgtcg ataaattcgt tacccttacc
151 gccgaaaagc agcctgccgt ccgcgctgag gcggtataaa tccaaaatat
201 ggcggttgct gcatactgcc atattgttgc ggataagccc ttttgtgcgc
251 gcgccaagg gttcgggtgc aataataaag gtgctgacgg caatcgctt
301 gcgttccaaa ggccggaata tcgggttcaa accgacataa gtattgacgg
351 catagaccac atttttacac tcgacgctgc cttcgggctg gtaaacacgc
401 caaccgtttt gatacgggtc gatgcgcgtc atcggggatt gctcgaaaat
451 ctgcgcgcgc gcttcggcag cggcgctggc aacacccaac gtgtaattga
501 gcggatgaag atgcccggac aagggatcga actgtgcgcc ttggtacata
551 tcgctgtcaa gctgctgttt caactcggct ttatcccaaa gttgataatg
601 actcgaccgc taatgcccgt ggcgctgttc atgccactgc tgcaactctt
651 cccaatgctg cggacggacg gcaaccgtgg cataaccgcg ctgccaatcg
701 caatcgatgg catgtttgcg gacgcgttcg tccaccagtt cgaccgcctg
751 caaagactgt tgccaaaacc attgcgcctg ctccaagccg acctgttttt
801 caatttcccc cataccgcag gcgtagtcgc tgataacctg cccgccactc
851 ctgccggacg cgcggaagcc gatacgtgcg gcttccaaaa cgacggcttc
901 atgtccgtgt tccgccagcg gcaatgcggt acacaaaccg ctcaaaccgc
951 cgccgataat gcagggttgc gctttcagac ggcattggag tttcggataa
1001 acagtatgcg gattaaccga actaaaataa taagaaggca gatattcttg
1051 aaaatcaggg cgaatcattg tgtttgcttt atcgggtata ttttcggacg
1101 gaatgataca gactgtcggg ccatatcgtc caaacagaaa atcggttga

```

This corresponds to the amino acid sequence &lt;SEQ ID 882; ORF 237.ng&gt;:

g237.pep

```

1  MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51  AEKQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQGGG NNGADGNRL

```

541

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN  
 151 LRAGFGSGAG NTQORVIERMK MPQGIELCA LVHIAVKLLF QLGFIPKLIM  
 201 TRTVMPPLGVF MPLQLFPMPL RTDGNRGITA LPIDIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF  
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL  
 351 KIRANHCVCF IGYIFGRNDT DCRAISSXQK IG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq

1 ATGCGGGACA AGGTTGGCGG TAATGTGCGA CTCCCCGCCC CACGAATATT  
 51 CGATTTTGAC ATCGGCAAGC TCGGAAAAA CTTTAAGCAT ATCTTGGCGG  
 101 ACAAGCTCGG TCATaCGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC  
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAAATA TCCAAAATAT  
 201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGCG  
 251 GCGGTTCCAA GGCCGGAATA TCGGGTCAA ACCTGCATAA GTATTGACAG  
 301 GCGTTCCAAA GGCCGGAATA TCGGGTCAA ACCTGCATAA GTATTGACAG  
 351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTCCGGCGT GTAAACACAG  
 401 CAACCGTTT GATGCGGTTG GATGCACGTC ATCGGGGATT GCTCGAAAAT  
 451 CTGCGCACCG GCTTCGCGAG CGGCACGAGC GATGCCCAA GTGTAAGTGA  
 501 GCGGATGCA GGTGTCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA  
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG  
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT  
 651 CCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA  
 701 CAATCGACGG CATGTTTTCG GACGCGTTCG TCCACCAAGT CGACCGCCTG  
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT  
 801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCCGCCACTC  
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC  
 901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC  
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA  
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG  
 1051 AAAATCAGGG CGAATCATTG TGTGTTGCTT ATCAGGTGTA TTTTCGGACG  
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAwACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep

1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT  
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL  
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN  
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPKLIM  
 201 TRTVMPPLGVF MPLQLFPMPL RTDGNRGITA LPITIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRAET DTRGFQHNRF  
 301 MSLLRQGQCS AOTTQSAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL  
 351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH	TLRIVDKLVILTAEKQSAVRAE				
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH	TRRIVDKFVILTAEKQPAVRAE				
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPF	CARPQGFGRNNGGADSNRLAFQRPEYRVQTCISIDSIDH				
g237	AVIIQNMAVVAYCHIVADKPF	CARAQFGGNNKGADGNRLAFQRPEYRVQTDISIDGIDH				
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGT	SDAQSVSERMQVSGXGVELCP				



g237	I F T L D A A F G R V N Q P T V L I R F D A R H R G L L E N L R A G F G S G A G N T Q R V I E R M K M P G Q G I E L C A	130	140	150	160	170	180
m237.pep	LVHIAVKLLFQLGFIPKLI MTRTVMPLGVFMPLLLQLFPMLRTDGNRGITALPITIDGMFA	190	200	210	220	230	240
g237	LVHIAVKLLFQLGFIPKLI MTRTVMPLGVFMPLLLQLFPMLRTDGNRGITALPIAIDGMFA	190	200	210	220	230	240
m237.pep	DAFVHQFDRLQRLLPKPLRLLQADLFFNFPHPTAXVIADNL PATPSRAETDTRGFQHNRF	250	260	270	280	290	300
g237	DAFVHQFDRLQRLLPKPLRLLQADLFFNFPHPTAGVVADNL PATPAGRAEADTCGFQNDGF	250	260	270	280	290	300
m237.pep	MSLLRQGQCSAQTTQSAADDTGIGFQTALKEFRINSMRINRTEIIRRQIFLKIRANHCVCF	310	320	330	340	350	360
g237	MSVFRRQRQCGTQTQTAADNAGFGFQTALKEFRINSMRINRTKIIRRQIFLKIRANHCVCF	310	320	330	340	350	360
m237.pep	IRCI FGRNDTG CRAISSXQKIGX	370	380				
g237	IGYIFGRNDTDCRAISSXQKIGX	370	380				

a237.seq

1	ATGCGGGACA	AGGTTGGCG	TAATGTCGA	CTCCCCGCC	CACGAATATT
51	CGATTTTGAC	ATCGGCAAGC	TGCGGAAAA	CTTTAAGCAT	ATCTTGGCG
101	ACAAGCTCCG	TCATACGCG	GGGATGTGC	ATAAACTCTA	TTCCTTACC
151	GCCGAAAAGC	AGTCTGCCG	CCGCGTGAG	CGGTAATAG	TCCAAATAT
201	GACGGTTGTC	GCATACTGCC	ATATTGTTGC	GGTAAGGCC	TTTTGCAGC
251	GCGCCCAAGG	GTTCTGTGGC	AATAATAAG	GTGCTGACAG	CAATCGCCTT
301	GCGCTCCAAA	GGCTTGAATA	TCGGATTCAA	ACCGGCATAA	GTATTGACGG
351	CGTACACGAC	ATTTTGTGAT	TCGACGCTGC	CTTCGGGGAT	GTAACCAGC
401	CAACCGTTTT	GTAAGGTTT	ATGCGTATC	GATGGAGAAT	GCTCAAAAT
451	CTTCGTACCA	GCTTCGGCAG	CGGCGCGGGC	GATGCCAAC	GTGTAATTGA
501	GCGGATGGAG	ATGCCCGGAC	AAGGGATCGA	ACTGTGCGCC	TTGGTACATA
551	TCGCTGTCAA	GCTGCTGCTT	CAGTTTCAGT	TTATCCCGA	GTTGATAATG
601	AGTTGCACCG	TAATATTTT	GGGCGTGCTC	ATGCCATTGT	TGCAATCTT
651	CCCAATGCTG	CGAACGGAT	GCAACCGTGG	CATAACCGCG	TCGCCAATCG
701	CAATCAATGG	CATGTTTTCG	GACGCGTTGC	TCCACCAGTT	CGACCGCCTG
751	CAAGACTGT	TGCCAAAACC	ATTGCGGTTG	CTCCAAACCG	ACCTGTTTTT
801	CAATTTCTCT	CATACCGCAG	GCGTAATCGC	TGATAAAGCT	CCCGCCACTC
851	CGTCCCGACG	CGCCGAAACC	GATGCGCGCG	GCTTCCAACA	CACCGCTTTC
901	ATGTCCCTGC	TCCGCCAAGG	GCAATGCAGT	GCACAAACCA	CTCAATCCGC
951	CGCGGATGAT	ACAGGTATCG	GTTTTCAGAC	GGCATTGAAG	TTTCGGATAA
1001	ACAGTATGAG	GATTAACCGA	ACTGAAATAA	TAAGAAAGGCA	GATATTTCTTG
1051	AAATCAGGG	CGAATCATTT	TGTTTGCTTT	ATCGGGTATA	TTTTCCGACG
1101	GAATGATACA	GCGTGTGAG	CCATATCGTC	CAACACAGAA	ATCGGTTGA

a237.pep

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMTVV	AYCHIVADKP	FCTRAQGGFCG	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAAGFG	VNQPTVLIRF	NAYHGRMLKN
151	LRTSFGSGAG	DQORVIERME	MFGQGIELCA	LHVHIAVKLLQ	QFSVIPPELIM
201	SCTVIFLGLV	MPLLQFFPML	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLLPKPLRL	LQTDLFNFNL	HTAGVIADNL	FATPSRRAET	DTRGFQHNRF
301	MSLLRQGQCS	AQTTQSAADD	TGIGFQTALK	FRNSMRINR	TEIIRRQIFL
351	KIRANHCVCVF	IGYIFGRNDT	GCRATSSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEQSAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMVAVYCHIVTDKPFPCARPQGFRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	AVIIQNMVAVYCHIVADKPFCTRAQGFQGNKGADSNRLALQRLYRIQTGISIDGVHQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDAHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	IFAFDAAFGGVNQPTVLRFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFIPKLIMTRTMPLGVFMPLQLFPMRLTDGNRGITALPITIDGMEA					
a237	LVHIAVKLLQLFSVIPELIMSCTVIFLGVLMPLQLFFPMRLTDGNRGITALPIAINGMEA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLLPKPLRLQLADLFFNFPHXTAXVIADNLPATPSRRAETDTRGFQHNRF					
a237	DAFVHQFDRLQRLLPKPLRLQLDQLFFNFLHTAGVIADNLPATPSRRAETDTRGFQHNRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVCFF					
a237	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVCFF					
	310	320	330	340	350	360
	370	380				
m237.pep	IRCIIFGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSKQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttgccag cggcaatata
51  gatgctgcat atccccatta gtcattgcga cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctcgcggcag tgtaaaaaat cgggtttgcg ccgtccaaac
201 atttgatgca actgcggtcg gcccataact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gccccttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcagg ttttctcagc
601 cgtgcggatg aagcaggaaa actgatattg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caaggtcgcg
701 ttaatccttt tttacgggt tttcaagggg tagggattgg ggcaattaca
751 gacagtgcgg taagcccgtg cacagataca gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtc ggaagcaca cttgccgccg

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcaggtag gggtttggcg ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcgga aggaaaagct aatgctgcaa
1151 cctatcctaa gttgggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaatTTTga aacttTact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAIISMLH IPISHANGLD ARLRDDMQAK HYPEPGGKYHL
51 FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPO APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFILTG FQGVGIGAIT
251 DSAVSPVTDI AAQQTLOGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHFN ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYT IDSNEKRNI KNGHLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTAAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAA GCACTTCTGA
351 TTTGAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTTCATCGAA
401 CAGGGTCCGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGACTAATAT TGTCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTTG CCGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACAA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCCAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAaaaaaag
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCGTGATA
1251 AGTTAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCAG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEPGGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

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545

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151 DYPPFGGARD IYSYYVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
301 AKQWADAHFN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMQTL DGEMAGGNKP IKSLPNSAAE KRKQNF EKFN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLQGGKQAKD YLQQQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238.pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAASMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCVAVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNHSDSKSTSDFSG					
	70	80	90	100	110	120
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPFGGARDIYSYYVKGTS TKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGGYPEPQGARDIYSYHIKGTSTTKINTVPQ					
	130	140	150	160	170	180
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
	250	260	270	280	290	300
m238.pep	310	320	330	340	350	360
	AKQWADAHFNITATAQTALS AAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL					
g238	ARQWADAHFNITATAQTALAVAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTV					
	310	320	330	340	350	360
m238.pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAEKRKQNF EKFN SNWSSASFDS VHKTLPNAP GILSPDKVKT					
g238	DGEMAGGNRPKSI - TSEGKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
m238.pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLD SNGNAVKTGNLQGGKQAKDY LQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTS GGGWLSRDGTRQYRPPTEKKSQFATTG IQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
1  ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51  GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCTG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTGTA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GCGGTAGACG GTGGTTTAC CGTTTACCAA CTTTCATCGGA
401 CAGGGTTCGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACTTCA ACAAAAACAA AGAGTAATAT TGTTCCCCGA GCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCAG TAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAATAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TAAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
1  MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51  FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQTLQGIN HLGNSPEAQ LAAATALQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAATTVWG GKKVELNPTK WDWKNTGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

m238.pep	10	20	30	40	50	60
	MNLPIQKFMM LFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
a238						
	10	20	30	40	50	60
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHDSKSTSDFSG					
a238						
	70	80	90	100	110	120
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGSTKTNTNIVPQ					
a238						
	130	140	150	160	170	180
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDIRGIVQGAVNPFLMG					
a238						
	190	200	210	220	230	240
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQTLQGINDLGKLSPEAQLAAASLLQDS AFAVKDGINS					

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|||||
a238      FQGVGIGAITDSAVSPVTDAAQQTLOGINHLGNLSPEAQLAAATALQDSFAVKGINS
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHPNITATAQTALSAEEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMTL
          |||
a238      ARQWADAHPNITATAQTALAVEAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRRQNFEKFNSSNWSSASFDSVHKTLPNAPGILSPDKVK
          |||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttcacc ataaaggat tgcccgaac cggcggatgg aggttttgtt
51  tttctgccc cgccctgat gcttcgtgat tcgccaacg cgccgtgttc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacggt tttctctgtt attattccgg tatcggaccg
301 gcagtcgctt cgcgcacacg caaaactgcg ctctcgcgcc tcgggttggt
351 ggcaatttcc gcttcacccg gctttaatgc cctgcccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg cgcgccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgccc gccctcttcc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttataaag
601 atgcggtatg cctggaaggt gcgcgtcgca ggatcctgcc cccgctcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaat ctggcgggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLR II LLQGDFLFFR
51  LVQSCEVEPV LVLLHHNGKS GNAHRKQKE IRFVHCRSDV FLCYYSIGIP
101 AVRSATR KTA LLALGLAAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR L
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCgAAAC CGGCKGATGG AGGTTTGTG
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAACCCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCG GCCTCACCCG GCTTTAATGC CCGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCACG CGGCAGGGG
451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GATCTTCAA
501 CGAATGGAAA GCAATGACCG CCAACGTCG GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGACG TTTTGTGCCA CGATCTGCGC CAGCTTGGCG GTTGATATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CCGCGGCTa
751 AACCCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

548

m239.pep  
 1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLRIT LLOGDFLFFR  
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQKE IQFVHCHSDV FLCDCSGIGP  
 101 AVRSATRKT LALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG  
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK  
 201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIIGLSARC ATMARAIRRL  
 251 NRSSP\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRITLLOGDFLFFRLIQSCEIEPV					
g239	MFHHKGIARNRMEVLFFCRRPDRFVIRQTRLLQPHLRITLLOGDFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQKEIRFVHCRSDVFLCYYSIGIPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIRRLNRSSPX					
g239	ATMARTIWRNLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq  
 1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTGTG  
 51 TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC  
 101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTCGCG  
 151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTCG TGCAATCACA  
 201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG  
 251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCGGG TATCGGACCG  
 301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC  
 351 GGCAATTTCG GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG  
 401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGGC  
 451 GCGTGTTCGG AATATTTTTC GACAACTGC TTCACAATGC GGTCTTCCAA  
 501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA  
 551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG  
 601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG  
 651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTGCGG GTTGATCGA  
 701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA  
 751 AACCGCTCTT CACCATAA

549

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLR II LLQGDFLFFR
 51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKT LALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLR ILLQGDFLFFRLIQSCEIEPV					
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLR ILLQGDFLFFRLIQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
a239	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
a239	ASPGFNALPAIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
a239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIIRRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacatatt cttcggcgcc gaaacgcgca gacagtttgc
 51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacat gggatcatc gcgcacggga gacggtccga tttataagg
151 ctgcgtattc agccgttcgt tcaaatcggg ttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
251 acggcacggg tgcgcgcgtg ttgcgtgtct gcccggccgg gtctgttggg
301 atcgtaggcg ggcgtatttg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcgg gcttttgctt gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgcggg tcccgcacaa caacttcgcg gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttcct gacctttgce
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacagggtg cccatcgggt
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
 51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNFR AVFAIQAVFK RKFQTFLTFA
```



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201 VNIGKSDDVC KQVAHRVMAF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

m240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTACAG CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCGGGCT TTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGGC CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGCTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 902; ORF 240&gt;:

m240.pep

```

1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFDCTRGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFAX RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFTFLTFVAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

m240/g240

	10	20	30	40	50	59
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMG I-AHGRRSDFIRLRIQPFVQIG					
	:     :     :     :     :     :					
g240	MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMG IIAHGRRSDFIRLRIQPFVQIG					
	10	20	30	40	50	60
	60	70	80	90	100	110
m240.pep	FARIQCLRNHHRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGEDFPRAGIQXH					
	:     :     :     :     :     :					
g240	FARIQCLRNHERFDCRTRFDHIGYGTVAPLFAVCPAGSVGIVGGRIQGEDFPRAGIQNH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m240.pep	HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFAXRGVQAVHNIALPVPQNDFR					
	:     :     :     :     :     :					
g240	HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNNFR					
	130	140	150	160	170	180
	180	190	200	210	220	
m240.pep	AVFAMQAVFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	:     :     :     :     :     :					
g240	AVFAIQAVFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAF					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

a240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTACAG CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

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```

251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1  MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGQED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQND FRA VFAMQAVFKR KFQTLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH	IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF				
	10	20	30	40	50	60
m240.pep	ARIQCLRNHHRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGQEDFPRAGIQXHH					
a240	ARIQCLRNHHRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGQEDFPRAGIQNH					
	70	80	90	100	110	120
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQND FRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQND FRA					
	130	140	150	160	170	180
m240.pep	VFAMQAVFKRKFTLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFTLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTC AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCAGAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1  MPTRPTRAAN PPTPTWLQT AYCPRPYRP PSVQTHPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPS C RQSVVVM TVR
101 TVDM TVCD FL IG CIAHAFNR S FKAD FHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTTCCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTCTTT CGGTTTGTG CAAAAGCTGA TTGTTGGCAT CATACATCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVVM TVR AVDM TVCD FL IG CIAHAFNC SLKAD FHACQ RMVAVHHRLA
51  VGNIGYTIDD NIAGFRIVGF KKHADFDNR EHARIFD TDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng)

from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVVM TVRAVDM TVCD FLIG CIAHAFNC		
				:		
g241	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPS	CRQSVVVM TVR	IVDM TVCD FLIG	CIAHAFNR
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKAD FHACQ RMVAVHHRLA VGNIGYTIDD NIAGFRIVGF KKHADFDNR EHARIFD TDQ				
		:       :       :       :       :       :       :       :				
g241	SFKAD FHACQ RMVAVHHRLA	VGNIGYTIDD	NIAGFRIVRF	KKHHTDLDFNR	ERARIFNTDQ	
	130	140	150	160	170	180
m241.pep		100	110	120	130	140
		LRILLAERIVGRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL				
		:       :       :       :       :       :       :				
g241	LRIMLTERIVGRKRHFDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV	QKLIVGIIHL	
	190	200	210	220	230	240
m241.pep		160	170			
		IMQRNHGIFH DSHICPFRNS		RLITGAFX		
		:				
g241	IMQRNHGIFC	NSHICPFRNS	RLITGAFX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACTCG CGCCGCAAAG CATCCAACCC CGCCAACTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAATCA
151 GCGAACCACG GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

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251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACACGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
1  MPTRPTRA AK HPTPPTWLQT AYCPRPFPYR PSVQTHTEPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPPSC RQSVVVMVTVR
101 TVDMTVCDL IGCIAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

m241.pep                                10      20      30
                                      RQSVVVMTVRAVDMTVCDFLIGCIAHAFNC
                                      |||||:|||||:|||||:|||||:
a241      QPTYLLHPSNKMPSMEQTLFRRHQIPPPSCRQSVVVMVTVRTVDMTVCDFLIGCIAHTFNR
              70      80      90      100     110     120

              40      50      60      70      80      90
m241.pep    SLKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFDSTDQ
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      SLKADFHACQRMVAVHHRLTVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFNTDQ
              130     140     150     160     170     180

              100     110     120     130     140     150
m241.pep    LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a241      LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              190     200     210     220     230     240

              160     170
m241.pep    IMQRNHGIFHDSHICPFRNSRLITGAFX
              |||||:|||||:|||||:|||||:|||||:
a241      IMQRNHGILHDSHICPFRNSRLITGAFX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTC AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CCGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGCTGCCC CGGCCGGGCC TGTTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGGCCTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGTTGCCC ATCGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

554

## g241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYP PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDFL IGCIHAHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

## m241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCTGCAAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGC GG
301 GCGGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CCGATTTCAT TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCTG
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CCGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCCCTT CAGGAACAGC AGATTAAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

## m241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYP PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 AVDMTVCDFL IGCIHAHAFNC SLKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADDFDNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFC
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pap	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pap	QPTYLLHPSNKMMPSETEQLFRRHQIPPSCRQSVVMTVRVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMMPSETEQLFRRHQIPPSCRQSVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pap	SLKADFHACQRMVAVHHRLAVGNIGYTIDDDNIAGFRIVGFKHHADDFDNRERARIFDQDQ					
g241	SFKADFHACQRMVAVHHRLAVGNIGYTIDDDNIAGFRIVRFKHHTDLDFNRERARIFDQDQ					
	130	140	150	160	170	180
m241-1.pap	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pap	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

## a241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCGCAAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

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101 AAACGCATAC ACCGCATGAA CCGGCTTCTT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAAC AAAATGCCGT CTGAAATGGA ACAAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTCCTA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRAAK HPTPPTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVVMTVR
101 TVDMTVCDFL IGCIHTFNR SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRAAKHPTPPTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSQSVVVMTVRAVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSNKMPSEMEQLFRRHQIPPSQSVVVMTVRTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVHRLAVGNIGYTIDNINAGFRIVGFKHHADFDNREHARIFDNDQ					
a241	SLKADFHACQRMVAVHRLTVGNIGYTIDNINAGFRIVGFKHHADFDNREHARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt ttgttcgtg atcgagcact tcaagcaacg
51  cgctggcgcg atcgccccga aagtcgctgc ccaatttgct gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct ttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 tttcgctcg cagccgccc aaggccatac ggacatattt ccgccccgtt
251 gctttggcga tggattcgcc caaagaggtt ttgccacgc ccggagggcc
301 gaccaaacac agaatcgga ctttgagctt gtccatacgt ttttgacgg
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcggc tttggcgatg tctttgctga cgcgggattt
451 tttcttcac ggagtcgga gcagggtgct gatgtagttg cgtacgacgg

```

556

```

501  tggattcggc agacatcggc ggcattcattt tgagtttttt cagttcggac
551  aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601  ctccaaggca tccagttcgc cgttttcgctc ttcttcgccc aattccttgt
651  gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701  atttggcggt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751  gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801  cgggaatctc caaaatctgt tggcggttgc ccagtttcaa ctgcaaatgc
851  gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pep

```

1  MIGELVVLFFV IEHFKQRAGG IAPKVAQFV DFVEQEQRVS YACFCHILQN
51  LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFDGF A QRGFAHARRA
101 DQTQNRTEFEL VHTFLDGEVF QNPFFDFFQA VVVGIQHQS FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRHHFEFF QFGQAFFFR FGHTRLFDAC
201 LQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

```

1  ATGATCGGCA AACTTGTTGT TTTGTTCCGG ATCGAGCACT TCGAGCAACG
51  CGCTGGCGGG ATCGCCTCGG AAGTCGTAC CCAATTGTC GATTTCGTCG
101 AGCAGGAACA AGGGGTTTTT CACGCCGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTCGC
201 TTTCTGTCGC CACGCCGCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTCCGC CAAAGAGGTT TTGCCACGCG CCGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATT
451 TTTCTTCCAC GGCAGCTCGA GCAAAGTGTG GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTTC TTCAGATAAT ATTCGCGCTG GGATTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGGAATTTC CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAATGC
851 GCTGCGACCG TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242.pep

```

1  MIGKLVLVLF IEHFEQRAGG IASEVVTQFV DFVEQEQGVF HAGFCHILQN
51  LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGF A QRGFAHARRA
101 DQAQNRAREF VHTFLDGEVF QNPFFDFFQA VVVGIQHQS FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFELF QFGQAFFFR FGHTRLFDIC
201 FQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVLVLFIEHFEQRAGGIASEVVTQFVDFVEQEQGVFHAGFCHILQNLTGHRADIGA					
	:          :      :  :          :       :     :					
g242	MIGELVVLFFVIEHFKQRAGGIAPKVAQFVDFVEQEQRVS YACFCHILQNL LAGHRADIGT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGF A QRGFAHARRADQAQNRAREFVHTFLDGEVF					
	:     :     :     :     :     :     :     :     :     :     :					
g242	AVPADFAFVAHAAQGHDTIFPPRCFGDGF A QRGFAHARRADQTQNRTEFELVHTFLDGEVF					
	70	80	90	100	110	120

	130	140	150	160	170	180
m242 . pep	QNPFFDFPQAVVVGIQHQSGFGDVFADAGFFLPRQLEQSVDDVAYDGGFRRHRWHHFELF					
g242	QNPFFDFPQAVVVGIQHQSGFGDVFADAGFFLPRQSEQVDVVAYDGGFGRRHRHHFEFF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFFGHTRLEDFICQGIQFAVFVFVFAQFFVYRNFNFVQIIIFALGFFHFLAFDAS					
g242	QFGQAFFFRFFGHTRLEDFICQGIQFAVFVFVFAQFFVYRNFNFVQIIIFALGFFHFLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVEFGFQLCQEQEFHPFADFGNLFQNLALLRQFQLQMRCDRIGX					
g242	AYAFFGLHNVEFGFQLCQEQEFHPFADFGNLQNLALLRQFQLQMRCDRIGX					
	250	260	270	280		

a242.seq

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242.pep

1	MIGELVVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQQWF	YAGFCHILQN
51	LTGHGADIFA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDQGA	QGFVAHAWRA
101	DQAGNRADIGE	VHTFLDFGEV	ONPFDFDQFV	VVVGIQHDSG	QRGVFADADG
151	FLPRQFEQGV	DVVAYDGGFG	RHRRHHFELE	QFGQAFFFRF	FGHTRLEFDC
201	FGGIQIAFVY	FFAQAFVYFR	NLFVQIIFAL	GFFHLAFDAS	AYAFFGLHNV
251	EGFGLCOQEE	FHPFADFGNF	QNLALLQRFQ	LQMRCDRIG*	

**m242/a242 95.2% identity in 289 aa overlap**

	10	20	30	40	50	60
m242.pep	MIGKLVVLF	GIIEHF	EQRAGGI	ASEVVTQ	FVDFVE	EQGVFHAGFCHILQNL
a242	MIGELVVLL	GIIKHF	EQRAGGI	AEVAXQ	FVDFVE	EQGVFYAGFCHILQNL
	10	20	30	40	50	60
m242.pep	AVSPDFAF	VAHAAQ	SHADIF	PPRCFG	DGDFAG	RGFAHARRADQAQNRAFEFVHTFLDGEVF
a242	AVSPDFAF	VAHAAQ	SHADIF	PPRCFG	DGDFAG	RGFAHAWRADQAQNRAFEFVHTFLDGEVF
	70	80	90	100	110	120
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150	160	170	180
m242.pep	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
a242	QNPFFDFF	QAVVVG	IIQHQS	GFGDVF	ADAGFF	LPRLEQSV
	130	140	150			



a242	QNPFFDFFQAVVVGIQHQS	SGFGDVFADAG	FFLPRQFEQGV	DVVAYDGGF	GFRHRHHFELF
	130	140	150	160	170 180
	190	200	210	220	230 240
m242.pep	QFGQAFFFRF	FGHTRLFDIC	FQGIQFAVF	VFFAQFFVYR	NLFVQIIFALGFFHLAFDAS
a242	QFGQAFFFRF	FGHTRLFDIC	FQGIQFAVF	VFFAQFFVYR	NLFVQIIFALGFFHLAFDAS
	190	200	210	220	230 240
	250	260	270	280	290
m242.pep	AYAFGLHNVE	FGFQLCQQE	FHPFADFGN	FQNLALRQF	QLQMRCDRIGX
a242	AYAFGLHNVE	FGFQLCQQE	FHPFADFGN	FQNLALRQF	QLQMRCDRIGX
	250	260	270	280	290

g243.seq

```
1 ATGGTAatcg tctGGTTGCC cgAGTTaccg CCGATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCAG CGATTTTTT gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGGGA AAGCGCGTGC AGAGGTTGAC GCGCAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCTCGCAA C TGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTC
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG
```

g243.ppe  
1 MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH  
51 IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF  
101 SSTTGAVTKS \*

```
m243.seq
1  ATGGTAATCG TCTGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCATACCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAAACGCG
101 CGATAACAGC GyTGGCGAGG AAGCGGGTGC AGAGGTTGAC GCGGACCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCACACAG GGGGCGAAyA GGTCTTCCTC
201 TTCCTGCAAA CCGCCATAT TCAGCATATC CCGTCCGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTGTGTT
301 TCACGTCCAG CAGGGCGGGT AACCAAGTCG TAG
```

m243.pep

1	MVIVWLPELP	PMPATMGISA	XSATIFSMLP	SNAPITRLAR	KAVQRLTASH
51	IQXFFTESHT	GANRSSSSCK	PAIFISISASD	SSRITSTISS	MVILEPMSFLE
101	SSTTGAVTKS	*			

Homology with a predicted ORF from *N. gonorrhoeae*

m243/g243

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSM	LPSNAPITRLARKAVQRLTASHIQXFFTESHT				
g243	MVIVWLPELPPMPATMGISAASATIFS	ILPSNAPMTRLARKAVQRLTASHIQRFLTESKT				
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSI	SADSSRITSTISSM	VILPMSFLFSSTTGAVTKSX			
g243	GANRSSSSCKPAMFNIS	ADSSRITSTISSM	VILPMSFLFSSTTGAVTKSX			

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1 ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1 MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFL
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIOXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVLPMSEFLSSTTGAVTKSX					
	:     :     :     :     :     :     :     :     :     :					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSVTLPMSFLSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1 atgccgcctg aagccccgcc ggcgggttca gacggcattg ccgctttact
51 tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcatcgctg atggatattc
251 ggatcgagct tatcgccgcg ttaggattg atttccttga tttgcgtggc
301 atcaaacgcc tcttgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgcatttc cagataatcc
401 ttgaccggca acattttcac ggcaaaactt tgtccggcga acttggtcgt
451 atcggaatt tctgctggtt ggcggcgccg caggttttgc tcgtttgcc
501 aagcgcgag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgtcat atcgtatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1 MPPEARPAGS DGIAALLRSV YTONALQEQI QIIPQTPSGF LPCHRNHSRA
51 QHTVGQGITL LHHTNHGIGF LLTGHRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

m244.pcp

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLPCHRNHSRAQHTVQGQITL					
	10	20	30	40	50	60
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRLLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	IAALIQRHFQIILDRQHFGKLLSGELVRI RNFLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQRHFQIILDRQHFGKLLSGELVRIGNFLVAAAQVLLVCQSAQLFVFQLRFQL					
	130	140	150	160	170	180
m244 . pep	GNPRLQILISRLCGSLFLHTVRI SYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRI SYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
g244	KSGYYPSKI RTFSRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCGGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAATTC TGTCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTCCAGCTC GGCAATCCGC
551 GCGTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTGC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAACAACAA TTGGAATCA AAATCCAGTT ATTACCGCG CAGATAAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLLVQVS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLLRHNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTONALQEI QIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQKRHFQIILDRQHFGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFTVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

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```

51  tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcy
151 caacacacgg teggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcaact gccacgcctt gcacgcctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttgctggc
301 atcaaacgcc ttctgcaact cattcaaatg catctgcaca cccattttca
351 gcgcacgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttccac ggcaaaactt tgccggcgga acttgtgcgt
451 atcggaatt tcctgctggt ggccggcgcg caggttttgc tcgttgcca
501 aagcgcgag ttgttctgtc ttcaactgcy cttccagctc ggcaatccgc
551 gcctgcgaat cctcataagc cggctcgcg gcagcctgtt cctgtacac
601 gtccgcattt cctactgtc cgaagggttc caccgcctcc acattttcaa
651 ccgctctctc actgttttgc tgcgtgtct gttcgctcat atcgatccc
701 tcaaaacaaa ttggaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaggcgag gaaatttcac atccgcgccc
801 gaatacccta ccgcaaaaac catataaacg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

```

g244-1.pep
1  MPPEARPAGS DGIAALLRSV YTONALQEQN QIIPQTSGF LPCHRNHSRA
51  QHTVGQGITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRFH QIILDRQHPH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFFVQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSGYPSKIR
251 TFSRNFQRQ EISHPPNTL PQPKYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

```

m244-1.seq
1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTCATCACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACGCGCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCGCG TTTAGGTTG ATTTCTCTGA TTTGCGTAGC
301 ATCAAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCAGC CCCATTTTCA
351 GCGCATCGAA ATTGCGGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCCGCGCA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GGCGGCGCGC CAGGTTTTC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTCTT GCACACCGTC
601 CGCATTTCTT ACTGTTTCGA CGGTTTCCAC CGCTCCACA TTTCAACCG
651 CTTCTTCACT GTTTGCTGCT TGTGCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAKCAGAGA ATTTCAAAAT CATTTTCAAA
801 TCCCTACCG AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

```

m244-1.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEQN QIIPQTSGF LLRHRNHSRA
51  QHAVGQRITL LHHTNHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRS
101 IKCFLLVQS HLHAHFQRIE IAALIQKRFH QIILDRQHPH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILIS LCGSLFLHTV
201 RISYCFDGFH RLHIFNRF VLLCLFAH VSLKTNWKSK SSYYPRKIRT
251 FSRNFQXQR ISNFSNPLP KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEQNQIIPQTSGFLLRHRNHSRAQHVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTONALQEQNQIIPQTSGFLPCHRNHSRAQHTVGQGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTNHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

```

a244-1.seq
1  ATGCCGCTGT  AAGCCCGACA  GGGCGGTTC  GACGGCATTG  CCGCTTTACT
51  TCGATCGGTT  TATACGAAA  ACGCGTTCA  GGAAATAAAT  CAGATTATT
101 CCCAGACGCC  TTCAGGCTTC  CTTCGTGCC  ACCGTAACCA  TAGCCGGGCG
151 CAACACCGGG  TCGGACAGCG  TATAACCCCT  CTTTCATCAG  CCCACACCGG
201 TATTGGGTCT  CTGTTGCTGT  GCCACGCCCT  GCATCGCCTG  ATGGATATT
251 GGATCGAGCT  TATCGCCCG  TTTAGGATTG  ATTTCTTGA  TTTGCGTAGC
301 ATCAATGCTT  TCTTGCAACT  CGTTCAAAGT  CATCTGCAGC  CCCATTTTAC
351 GCGCATGCTA  AATGGCCGTC  TGATCAAAA  GCGCCATTTC  CAGATAATTC
401 TTGACCGGCA  GCATTCCAC  GGCAAATCTT  TGTCCGGGCA  ACTTGTGGGT
451 ATCCGCAATT  TCTGTGCTGT  GGGCGCGCGG  CAGGTTTTCG  TCGTTTGCCA
501 AAGCGCGCAG  TCGTCGCTF  TTCAACTGCG  CTTCCAGCTC  GCGAATCCGC
551 GCCTGCAAA  CCTCATAAGC  CGGCTCTGCG  GCAGCCTGTT  CCTGCACACC
601 GTCCGCAATT  CTTACTGTCT  CGACGGTTTC  CACCGCCTCC  ACATTTTCAA
651 CGCTCTTCTC  ACTGTTTTGC  TGCTGTGTCT  GTTCGCTCAT  ATCGTATCCC
701 TTAARACAAA  GTGGAAATCA  AAATCCAGTT  ATTACCCGGG  CAAGATAAGG
751 ACATTTTCAA  GAAACTTTCA  GCAAAGGCAG  AGAATTTCAA  ATTCATTTTC
801 AAATCCCTTA  CCGAAAAAAT  AA

```

a244-1.pap

1	MPSEARQAGS	DGIAALLRSV	YTQNALQEIN	QIIPQTPSGF	LLCHRNHSRA
51	QHAVGQRITL	LHHAAHHGIGF	LFACHRLHRL	MDRIETIELR	FRIDFLDLRS
101	IKCFLQLQVS	HLHAHFQRIE	IAALIQKRHF	QIILDRQHFH	GKLLSGELVR
151	IRNFLVLVAA	QVLVLQCSAQ	LLVFLRFLQL	GNPRLQILIS	RLCGSLFLMT
201	VRISYCLDGF	HLRHILFNRF	TVLLLLCFAH	IVSLKTNWKS	KSSYPYPRKIR
251	TFSRNFKQRQ	RISNFSNPL	PKK*		

	10	20	30	40	50	60	
m244-1.pep	MPSEARQAGSDGIAALRSVYTQNALQEINQIIPQTSGFLLRHRNHSRAQHAVGQRITL						
a244-1	MPSEARQAGSDGIAALRSVYTQNALQEINQIIPQTSGFLLRHRNHSRAQHAVGQRITL						
	10	20	30	40	50	60	
	70	80	90	100	110	120	
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE						
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE						
	70	80	90	100	110	120	
	130	140	150	160	170	179	
m244-1.pep	IAALIQRKHFQIILDRQHFGKLLSGELVRI RNFLLVAAAQVLLVCQSA-LLVFQLRFQL						
a244-1	IAALIQRKHFQIILDRQHFGKLLSGELVRI RNFLLVAAAQVLLVCQSAQLLVFQLRFQL						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m244-1.pep	GNPRLQILISRLCGSLFHTVTRISYCFDGFHRLHIFNRFVTLLCLFAHIVSLKTNWKS						
a244-1	GNPRLQILISRLCGSLFHTVTRISYCLDGFHRLHIFNRFVTLLCLFAHIVSLKTNWKS						
	180	190	200	210	220	230	240

564

	240	250	260	270
m244-1.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKXX			
a244-1	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKXX			
	250	260	270	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 941>:

```

g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgect tcgttttcga
51  ccagacacag cgtgcccgtt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgtctgta aatatcgcg agggctttgc gggcgaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgg tgtgccgagg ttttgggtgga
201 acagttcgct gacctgttct ttggttttat ggattgcggg catcacgata
251 tgggtcgggt tttcgccctgc catttgagcg ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggtt
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgcccc
451 gtgtactttc acgccaact tagtcagggt ttcttccaac tgctccagca
501 gcgcgggtaa

```

This corresponds to the amino acid sequence <SEQ ID 942; ORF 246.ng>:

```

g246.pep
1  MYGRNGSTQA AVAFVFDQTQ RARFGNGEVY AAQADIGSAV NIAQGFAGES
51  GQLVHVVCXR CAEVLVEQFA DLFFGFMDCG HHDGMGRFFAC HLDDKLAQVA
101 FHRLNAFCFK IMVQLDFFAD HGFAFDHQLA VFGCDDVVDN LAGFGRGFRP
151 VYFHAQLSQV FFQLLQQRG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 943>:

```

m246.seq (partial)
1  ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51  CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACTCAAAC
101 CGACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTACGCGGC GTACCGAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCAGATAT
251 GGGTCGGTTT TTCGCCTGCC ATTTGGACGA TGAAGTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGCyTTT TGCTTCAAGA TAATGrTTCA GCTCGATTTC
351 CTCGCTGACC ATCGATTGTC CTTTGACCAT CAGCTTGCCG TTTTGGCTG
401 TGATGATGTC GTGGATAATT TGGCAGGCTT CGGTCGGGGT TTCTGCCCG...

```

This corresponds to the amino acid sequence <SEQ ID 944; ORF 246>:

```

m246.pep (partial)
1  MHGRYGGTQA TVAFVFHQTO RTCFSNGKVY ATQTDIGSAV NIAQCFTGEA
51  GQLVYIVCQR RTEVLVEQFA NLFFGFVDSR HHDGMGRFFAC HLDDKLAQVA
101 FYRFNAFCFK IMXQLDFLAD HRFAFDHQLA VFGCDDVVDN LAGFGRGFCP...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

m246/g246

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQRTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
	:    : : :          : : :					
g246	MYGRNGSTQA AVAFVFDQTQ RARFGNGEVY AAQADIGSAVNIAQGFAGES GQLVHVVCXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDKLAQVAFYRFNAFCFKIMXQLDFLAD					
	: : : : : : : : :					
g246	CAEVLVEQFADLFFGFMDCGHHDGMGRFFACHLDDKLAQVAFHRLNAFCFKIMVQLDFFAD					

565

	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1  ATGCACGGGC  GGAACGGTGG  TACTCAAGCG  ACCGTTGCCT  TCGTTTTCCT
51  CCAGACACAG  CGTACCTGTT  TCAGCAACGG  CGAAGTTCAC  GCCACTCAAA
101 CCGACATCGG  CAGTGCTGTA  AATATCGCGC  AGTGCTTTAC  GGGCGAAGCC
151 GGTCAGTTGG  TCTACGTCGT  CCGTTAACGG  TGTGCCGAGG  TTTTGGTGGA
201 ACAGTTCGCT  AACCTGTTCT  TTGGTTTTAT  GGATTGCGGG  CATCACGATA
251 TGGGTCGGTT  TTTCACCTGC  CATTTGGACG  ATGAACTCGC  CCAAGTCGCT
301 TTCCACCGCT  TTAATGCCTT  TTGCTTCAAG  ATAATGGTTC  AGCTCGATTT
351 CCTCGCTGAC  CATCGATTG  CCTTTGACCA  TCAGCTTGCC  GTTTTGGCT
401 GTGATGATGT  CGTGGATGAT  TTCGCAGGCT  TCGGCCGGTG  TTCCGCCCA
451 GTGTACTTTT  ACGCCCAACT  TGTCAGGTT  TTCTCCAGC  TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1  MHGRNGGTQA  TVAFVFHQQT  RTCFSNGEVH  ATQTDIGSAV  NIAQCFTGEA
51  GQLVYVVR*R  CAEVLVEQFA  NLFFGFMDCG  HHDMMGRFFC  HLDDELAQVA
101 FHRENAFCFK  INVQLDFLAD  HRFAFDHQLA  VFGCDDVVDD  FAGFGRCFRP
151 VYFYAQLGQV  FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQQTQRTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMMGRFFTCCHLDDELAQVAFHRENAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
a246	HRFAFDHQLAVFGCDDVVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1  atgaaacgta  aaatgctaaa  cgtaccaaag  ggcgggttatg  atggtatgaa
51  gggttttacc  attgttgaat  ttctggttgc  gggcctgctc  agtataattg
101 tcctgatagc  ggtcgtatcg  agttacttta  catcccgga  attaaatgat
151 gtggcaaacg  agcgtcttgc  cattcaacag  gatttgcgga  atgcggcaac
201 attaattgtc  cgcgatgcaa  gaatggcggg  gagcttcggt  tgtttcaata
251 tgtccgagca  tactaaagac  gatattgttg  attcaagtaa  tcaaactcaa
301 tctaaccttg  caaaacccgg  tgccaaacaa  gaaaatcccc  ttttttcctt
351 aaaaaggagc  ggcattgata  aacaactgat  tcccgttgct  gaatccatag
401 atattaaata  tccgggtttt  atccagcgcc  ttaacgcatt  ggttttccaa
451 tacggtatcg  atgatcttga  tgcgagtgc  gagactgttg  tagtcagcag
501 ctgttccaaa  atagcaaaac  cgggtaagaa  aatatctacc  ttgcaagaag
551 caaagagtgc  attacagatt  actaatgatg  ataacaacaa  tggaaatc

```



q247.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

```

seq      (partial)
1         ATGAGACGTA  AAATGCTAAA  CGTwsyArAA  GGCAGTTATG  ATGGTATGAA
51        AGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCCTGCTC  AGTATGATTG
101       TCCTGATGCG  GGTCCGATCG  AGTTACTTCA  CATCCCCGAA  ATTAATATGAT
151       CGGGCAAACG  AGCGTCTTGC  CGCGCAACCA  GATTTCGGGA  ATGCGGCAAC
201       ATTGATTGTC  CGCGATGCGA  GAATGGCAGG  CGGCTTCGGT  TGGTTCAATA
251       TGTCCGAGCA  TCCTGCAACT  GATGTTATTC  CCGATACGAC  GCAACAAAAT
301       TCTCCTTTT  CCTTAAAAAG  GAACGGTATA  GATAAACTTA  TTCCCATAGC
351       GGAATCTTCA  AATATCAATT  ATCAGAATTT  TTTCCAGGTT  GGTAGCGCAT
401       TGATTTTTCA  ATACGGAATC  GATGATGTTA  ATGCAAGCAC  CGCGCATACC
451       TCGTGCAGCA  GCTGTGCGCG  AATATCGAAA  CCGGGCAAGC  AAATCCCTAC
501       TTTAGAAGAT  GCAAAAAAAG  AATTGAAGAT  TCCGGATCAG  GATAAGGAGC
551       AAAATGGCAA  TATAGCGCGT  CAAATGGCAT  TGGTCAATGC  TTATGCGGTC
601       GGCAGGATTG  CCGATGAGCA  AAGTTGTCTT  CGTTCCAAT  TGGATGATAA
651       GGGCAAGTGG  GGTAATCTCT  AGTTGC...

```

m247.pep (partial)

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng)

from *N. gonorrhoeae*:

m247/q247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAA	NERLAAQQ				
	: : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
g247	MKRKMLNVPKGGYDGMKGFTTIVEFLVAGLLSIIVLIAVVSSYFTSRKLNDV	ANERLAIQQ				
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSP	FLSKRN				
	: : : : : : : : :	: : : : : : :	: :	: :	: :	: : : : : : :
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKENP	FLSKRS				
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIPIAESSNINYQNFFQVGSALIFQYIGDDVNASTATTVVSSCAA	ISKPGKQIPT				
	: : : : : : : : :	: : : : : : :	: :	: :	: :	: : : : : : :

```

g247      GMDKQLIPVAESIDIKYPGGFIQRLNALVFQYGIDDLDAETAETVVVSSCSKIAPGKKIST
           130         140         150         160         170         180

m247.pep  170        180        190        200        210        220
          LEDAKKELKIPDQKEQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWGNPQL
          |::||:|: ||:|| ||||:||||:||||:||||:||||:|::|
g247      LQEAKSALQITNDDK-QNGNITROKHVVNAYAVGRFGNNEESLFRFQLDDKGKWGNPQLL
           190        200        210        220        230

g247      VKKVKRMDVRYIYVSGCPEDEDAGKEEFRTYNKFDSKNNAVTPAGVEVLLEDGLNAKIA
           240        250        260        270        280        290

```

```

a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCTGTATGGC  GTTCCGATCG  AGTTACTTCA  CATTCCGGAA  ATTAATGATG
151 GCGGCAAACG  AGCGTCTTTC  CGCGCAACAG  GATTTGCGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAACT
301 CAACATGTCC  GTGTAAAACC  CGGTGCCAAA  CAGAAAAATC  CCCTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGGATGC
501 TGAGACTGTT  GTAGTCAGCA  CGTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTGCGC  AGGATTGCCG  GTGAGGAAGT  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCTCAGT  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTTGTGTTCC  GACTGTCTGT  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATT  GACAGCTCCA
851 CAAATGCTGT  TACGCCCGCC  GGGGTGGAGT  TTTATTAGAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAAT  CATTATTATG  CTTACCGTAT
951 CGATGCGACA  ATACGCGGGG  GAATGTATG  CGCAACAGA  ACACTTTGA

```

a247.pep

1	MRRKMLNVPK	GNYDGMKGFT	IEFLVAGML	SMIVLMAVGS	SYFTSRKLND
51	AAANERLSAQK	DLRNAATLIV	RDARMAGGFG	CFNMSEHTKN	DIIVDPSPKQT
101	QHVPVKPAQK	QENPLFSLEW	ANTNTNNNT	AKLIPIAEST	DIKYPGFAQA
151	RPALIFQYGI	DDLDAEAETV	VVSSCSKIAK	PGKKISTLQE	AKSALQITND
201	DKQNGNITRQ	RHVVNAYAVG	RIAGEEGLFR	FQLDDKGKWG	NPQLLVKKIR
251	HKVQVRYIYS	DCPEDDDAGK	EEKFKYTGTF	DSSTNAVTPA	GVEVLLSXGT
301	DTKIAASSDN	HIYAYRIDAT	IRGNGVCANR	TL*	

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ					
		:	:	:	:	:
a247	MRRKMLNVPKGNYDGMKGFTTIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONSPPFSLK-					
			:		:	
a247	DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTQHVVPVKPGAKQENPLFSLEW					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAIISK					
	:		:	:	:	
a247	ANTNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDASETVVVSSCSKIAK					
	130	140	150	160	170	180

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	170	180	190	200	210	220
m247.pep	PGKQIPTLED	AKKELKIPDQ	KEQNGNIARQ	RHVVNAYAVG	RIADEESLFR	QLDKDGKW
	:	: :	: :	: :	: :	: :
a247	PGKKISTLQ	EAKSALQIT	NDDK-QNGN	ITRQ	RHVVNAYAVG	RIAGEEGLFR
	190	200	210	220	230	
m247.pep	GNPQL					
a247	GNPQLLVKK	IRHMKVRYI	YVSDCPEDD	DAGKEEKFKY	TGTFDSSTNA	VTAGVEVLLS
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1   CCCGGTGCCA AACAGAAAA TCCCCTTTT TCCTTAAAA GGAGCGGCAT
51  GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAGAA GGTTAAACGT ATGGATGTGC GGTATATTTA TGTTCCGGT
451 TGTCCTGAAG ATGAAGATGC CGGCAAGAG GAAAAATCA GATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTAC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGCGACAATA CGCGGGGAA ATGTATGCGC
651 AACAGAACCA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1   PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYIDDD
51  LDASAETVVV SSCSKIAPG KISTLQEAK SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFRF QLDDKKGWGN PQLLVKKVKR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIAASSDNS
201 IYAYRINATI RGGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1   ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTACC ATTATTGAAT TTTTGGTTGC GGGCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAABAC AGCGTCTTGC CGCGCAACAG GATTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTTCAATA
251 TGTCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAT
301 TCTCCTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTC AATACGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTGAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAAATGC
801 TGTTACGCCC GCCGGGTGAG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1   MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLN
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQON
101 SPFSLKRNGI DKLPIAESS NINYQNFFQV GSALIFYQYI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEGLF RFQLDDKKGW GNPQLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIIAYRIDA
301 TIRGGNVCAN RTL*

```

	70	80	90	100	110	120
m247-1.pep	NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQQNSPFFSLKRNIGDK-LIPIAESSNI					
				:   :       :   :       :		
g247-1	PGAKQENPLFSLKRSMDKQLIPVAESIDI					
				10	20	30
	130	140	150	160	170	180
m247-1.pep	NYQNFFQVGSALIFQYGIDVDNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK					
	:   :   :   :         :   :   :   :   :   :   :   :   :					
g247-1	KYPGFIQLNALVFQYGIDDLDAEETVVVSSCSKIAKFGKKISTLQEAKSALQITNDKK					
	40	50	60	70	80	90
	190	200	210	220	230	240
m247-1.pep	EQNGNIARQHRVVNAYAVGRIAD-EEGLFRFQLDDKGKNGNPQLLVKKVRHMKVRYIYVS					
	:   :   :   :   :   :   :   :   :   :   :   :					
g247-1	-QNGNITRQKHVVNAYAVGRFGNGNEESLFRFQLDDKGKNGNPQLLVKKVRMDVRYIYVS					
	100	110	120	130	140	
	250	260	270	280	290	300
m247-1.pep	GCPEDDDAGKEETFKYTDKFDQAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT					
	:       :   :   :   :   :   :   :   :   :   :					
g247-1	GCPEDDEDAGKEEFRTYTNKFDKSKNAVTPAGVEVLLDGLNAKIAASSNSIYAYRINAT					
	150	160	170	180	190	200
	310					
m247-1.pep	IRGGNVCANRTLX					
g247-1	IRGGNVCANRTLX					
	210	220				

a247-1.seq	(partial)						
1	AAATATACAG	CTAAATTGAT	TCCTATTGCT	GAATCCACAG	ATATTAAATA		
51	TCCGGGTTTT	GCCCAGGCTC	GTCGGGCATT	GATTTTCCAA	TACGGCATCG		
101	ATGATCTTGA	TGCGAGTGCT	GAGACTGTTG	TAGTCAGCAG	CTGTTCCAAA		
151	ATAGCAAAAC	CGGGTAGAA	AAATATCTACC	TTGCAAGAAG	CAAAAGATGC		
201	ATTACAGATT	ACTAATGATG	ATAACAAAA	TGGAATATC	ACCCGTCAAA		
251	GGCATGTGGT	CAATGCCTAT	CGCGTCGGCA	GGATTGCCGG	TAGGAGGAAGT		
301	TTGTTCCGCT	TCCAATTGGA	TGATAAGGGC	AAGTGGGGTA	ATCCTCAGTT		
351	GCTCGTGAAA	AAGATTATAG	ATATGAAAGT	CGGGTATATC	TATGTTTCCG		
401	ACTGTCCTGA	AGATGACGAT	GCGGCGCAAG	AGGAAAAAAT	CAAAATATATC		
451	GGTACATTGC	ACAGCTCCAC	AAATGCTGTT	ACGCCGCCCG	GGGTGGAGGT		
501	TTTATTGAGT	AGCGGTACTG	ATACCAAGAT	TGCCGCTTCT	TCAGACATTC		
551	ATATTTATGC	TTACCGTATC	GATGCGACAA	TACGCGGGGG	AAATGTATGC		
601	GCAAAACAGAA	CACTTTGA					

a247-1.pep (partial) ..

1	NNTAKLPIA	ESTDIKYPGF	AQARAPALIFQ	YGIDDLDSA	ETVVVSSCSK
51	IAPKPKKIST	LQEAASALQI	TNDDKQNGNI	TRQRHVVNAY	AVGRAGEEG
101	LFRFQLDDKG	KWGNPQLLVK	KIRHMKVRYI	YVSDCEDDD	AGKEEKFKYT
151	GTFDSSTNAV	TPAGVEVLLS	SGTDTKIAAS	SDNHIYAYRI	DATIRGGNVC
201	ANRTL*				

[illegible]

570

```

m247-1      YAVGRIADEEGLFRQLDKKGWGNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFYK
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1  atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgcccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa tttcagggtt tggatttggg atatgctgag gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgagg caggcgtag caaaatgccg cgctatatta tcgaatattt
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1  MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSSEA FGNIVQGKP AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIYLGVK NGQNVYRVT AKAQKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1  ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.Tywt
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGCTT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAACTGTG GAAAAGGTCT GtTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTT ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAAATGTTT ATCGGTTTAC TGCCAAGGCT TGGGGAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1  ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXR
51  EGELQVLDLE YTDTSKVTFE ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXKEYKKG TRSVTKMPRY IIEYLGXNG
151 ENVYRVTAKA WGNANTVVV LQSYVSNDE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
              GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
              | | : |||| | || | | ||||| ||||| ||||| |||||

```

571

```

g248      MRKQNTLTGIPTSDGQSGSALFIVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :||||||| :||| |||||
g248      LAEAAALREGFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70      80      90      100     110     120

           110     120     130     140     150
m248.pep  TVEAVKRSCPA---NSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLVGXNGENVYRVTA
           :||||||| :||||||| ||:|: :|: ||||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLVGXNGENVYRVTA
           130     140     150     160     170     180

           160     170     180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           ||| ||||| ||||| |||
g248      KAWGKNANTVVVLQSYVGNINDEX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACAACCTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAAACGTG GAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCAAC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCTG CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLVGXNGENV YRVTAWGWK NANTVVVLQS YVSNINDEX*

```

m248/a248 89.4% identity in 180 aa overlap

```

           10      20      30      40
m248.pep  GFALLIVLMVXIVVAFXXVTAQSYNTEQRISXNESDRKLAXS
           |||:||||| ||||| ||||| ||||| ||||| |||||
a248      MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEAAALREGELQVLDLEYDTSKVTFSENCGLCTAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100     110     120

           110     120     130     140     150     160
m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLVGXNGENVYRVTAWGWK
           ||||| ||:| ||||:| |||||:|: ||||| ||||| ||||| |||||
a248      VEAVKRSC TAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLVGXNGENVYRVTAWGWK
           130     140     150     160     170     180

           170     180
m248.pep  NANTVVVLQSYVSNINDEX

```

572

|||||  
a248 NANTVVVLQSYVSNINDEX  
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq  
1 ATGCGCAAAC AGAACAACCTTT GACGGGAATC CCGACTTCTG ACGGACAGAG  
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT  
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC  
151 AACGAATCAG ACAGGAAAT GGCCTTGTCT TTGGCCGAGG CGGCTTTGCG  
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG  
251 TTACATTTAG CGAAAACGTG GGAAAAGGTC TGTGTGCCGC AGTGAATGTG  
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG  
351 CAAGCCACCC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG  
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC  
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG  
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA  
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep  
1 MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA  
51 NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV  
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCPA NSTDLCDKK GMEYKKGTRS  
151 VSKMPRIIE YLGVKNGENV YRVTAKEWK NANTVVVLQS YVSNND\*

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQKGP					
g248	LAEALREGE LQVLDLEYAADS KVTFSENC GKGLCTAVNVRTNNGSEAFGNIVVQKGP					
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA----NSTDLCDKKGMEYKKGTRSVSKMPRIIEYLGVKNGENVYRVTA					
g248	AVEAVKRSCPAKSGKNSTDLCDKNKGMEYKKAAGVSKMPRIIEYLGVKNGQNVYRVTA					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNINDEX					
g248	KAWGKNANTVVVLQSYVGNINDEX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQKGP					
a248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCTAVNVRTNNDNEEAFDNIVVQKGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCDKKGMEYKKGTRSVSKMPRIIEYLGVKNGENVYRVTAKEWK					
a248	VEAVKRSCPAKSTDLCDKNKGMEYKKGTSVSKMPRIIEYLGVKNGENVYRVTAKEWK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

m249.pep MKKND C FRL KDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX  
| | | : | : | | | | | | | | | | | | | | | | | : : :



g249	MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTQIVTSQITQ	10	20	30	40	50	60
m249.pep	XLMEGMLMNPTIDSDSNKKNYNLYMGNHTLSAVDGDFAIDAMKTGQLAEAQKRFSEYEL	70	80	90	100	110	120
g249	NLMEGMLMNPTIDLDSDNKKNYSLYMGKQTLTSAVDGEFMILDAEKSQAQLAEEQKRFSEHLL	70	80	90	100	110	120
m249.pep	KNALPDAAAIHYAVCKDSSGNAPTLSGN-APSSNCDNKANGDTLIKVLVWVNSAGDSDIS	130	140	150	160	170	179
g249	KNALPDVAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLVWVNSAGDSDIS	130	140	150	160	170	180
m249.pep	RTNLEVSGDNIVYTYQARVGGREX	180	190	200			
g249	RTNLEVSGDNIVYTYQARVGGREX	180	190	200			

```
a249.seq
1  ATGAAGAATA  ATGATTGCTT  CCGCCTGAAA  AACCCCCAGT  CCGGTATGGC
51  GCTGATAGAA  GTCTTGGTCG  CTATGCTCGT  TCTGACCATC  GGTATTTTGG
101  CACTATTGTC  GTTTCAGTTG  CGGACAGTCG  CTTCCGTCAG  GGAGGCAGAG
151  ACGCAAACCA  TCGTCAGTCA  AATCACGCAA  AACCTGATGG  AAGGAATGTT
201  GATGAATCCG  ACCATTGATT  CGGCACAGCA  CAAGAAAAAC  TATAATCTTT
251  ACATGGGAAA  CATCATGCA  CTATCAGTTG  TAGTGGCGA  TTTTCAGGTT
301  GATGCCATAA  AAACAAAGAC  GCAGTTGGCA  GAGGCACAAT  TGAAGAGATT
351  TAGTTATGAG  CTGAAAAATG  CCTTGCCCGA  TCGCGGAGCC  ATCCATTACG
401  CCGTCTGCAA  GGATTGCTGT  GGTGTTGCGC  CGACATTGTC  CGCCGGCGAT
451  ACTTTTCTT  CAAATTCGCA  TGGTAGTGCA  AATGGGGATA  CTTTGATTAA
501  AGTATTGTGG  GTAAATGATT  CGGCAGGGGA  TTCGGATATC  GCCCGTACGA
551  ATCTTGAGAC  GAACGGCAAC  AATATCGTAT  ATACCTATCA  GGCAAGGGTC
601  GGAGGTGCGG  AATGA
```

a249.pep

1	MKNNDCEFRLK	NPQSGMALIE	<u>VLVAMLVLT</u>	<u>GILALLSVQL</u>	RTVASVREAE
51	QTQTVSQITQ	NLMEGMLMNP	TIDSDSNKNK	YNLYMGNNHA	LSVVDGDFQV
101	DAIKTKTQLA	EAQLKRSFYE	LKNALPDAAA	IHYAVCKDSS	GVAPTL SAGS
151	TFSSNCDCGSA	NGDTLIKVLW	VNDSAGDSDI	ARTNLETNGN	NIVVITYQARV
201	GGRE*				

	10	20	30	40	50	60
m249.pep	MKNNDCFR	LKDSQSGMALIEVLV	AMLVLTIGILALLSV	QLRTVXXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX
	:	:	:	:	:	:
a249	MKNNDCFR	LKNPQSGMALIEVLV	AMLVLTIGILALLSV	QLRTVASVREAETQT	IVSQITQ	
	10	20	30	40	50	60
	70	80	90	100	110	119
m249.pep	XLMEGMLMNPTIDSD	SNKKNYLYMGNH-TLS	AVDGDFAIDAMKTG	QLAEAL	KRFSYE	
	:	:	:	:	:	:
a249	NLMEGMLMNPTIDSD	SNKKNYLYMGNH	HALSVVDGDFQVDA	IKTKQLAEAL	KRFSYE	
	70	80	90	100	110	120
	120	130	140	150	160	170
m249.pep	LKNALPDA	AAIHAVCKDSSGNAPT	LS-GNAFSSNCDNKANG	DTLIKVLWVND	SAGDS	SDI
	:	:	:	:	:	:
a249	LKNALPDA	AAIHAVCKDSSGVAPT	LSAGSTFSSNCDGSANG	DTLIKVLWVND	SAGDS	SDI
	130	140	150	160	170	180

```

      180          190          200
m249.pep SRTNLEVSGDNIIVYTYQARVGGREX
           :|:|||::||:|||||
a249     ARTNLETNGNNIIVYTYQARVGGREX
           190          200

```

m249-1.seq

1	ATGAAGAATA	ATGATTGCTT	CCGCGCTGAA	GATTCCCAGT	CCGGTATGGC
51	GCTGATAGAA	GTCITGGTGT	CTATGCTCGT	TCTGACCATC	GGTATTTTGG
101	CACATATTGC	TGTACAGTTG	CGGACAGTCG	CTTCCGTCAG	GGAGGCGGAG
151	ACACAAACCA	TCGTCAGCCA	AATCACGCAA	AACCTGATGG	AGGGAATGTT
201	GATGAATCCG	ACCATTGATT	CGGACAGCAA	CAAGAAAAAC	TATAATCTTT
251	ACATGGGAAA	CCATACATA	TCAGCTGTGG	ATGGCGATT	TGCGATTGAT
301	GCCATGAAAA	CTAAGGGCCA	ATTGGCAGAG	GCACATATGA	AGAGATTTAG
351	TTATGAGTCG	AAAATGGCT	TGCCGGATGC	GGGACCCATC	CATTACGCCG
401	TCTGCAAGGA	TTCTGCGGTT	AACGCGCCGA	CATTGTCCGG	CAATGCTTTT
451	TCTTCAAATT	CGGACAATAA	GGCAAACGGG	GATACTTTAA	TTAAAGTATT
501	GTGGGTAAAT	GATTTCGGAG	GGGATTCGGA	TATTTCCCGT	ACGAATCTTG
551	AGGTGAGCGG	CGACAATATC	GTATATACTT	ATCAGGCAAG	GTCTGGAGGT
601	CGGGAAATGA				

m249-1.pap

1	MKNNDGFR	LK	DSQSGMALIE	VLVAMLVLT	I	GILALLSVQL	RTVASVREAE
51	TQTIVSQITQ		NLMGGLMNP	TIDSDSNKN		YNLYMGNHTL	SAVDGDFRID
101	AMKTGQLAE		AQLKRFSYEL	KNALPDAAAI		HYAVCKDSSG	NAPTLSGNAF
151	SSNCDNKANG		DTLIKVLWVN	DSAGDSISR		TNLEVSGDNI	VYTYQARVGG
201	RE*						

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMAL	IEVLVAMLVLTIGIL	ALLSVQLRTVASV	REAE	TQTIVSQITQ
g249		:				
	10	20	30	40	50	60
m249-1.pep	NLM	EGMLMNP	TI	DS	DSNKK	NYNLYMGNHTLSAVD
g249						
	70	80	90	100	110	120
m249-1.pep	GF	AFIDAMK	TKGQLAE	AQLK	RFSYEL	
g249						
	70	80	90	100	110	120
m249-1.pep	NLM	EGMLMNP	TI	DL	DSNKK	NYSLYMGKQ
g249						
	130	140	150	160	170	179
m249-1.pep	KNALP	DAAAIH	YAVCKD	SSGNA	PTLSGN	-AFSSNCDNKANGDT
g249						
	130	140	150	160	170	180
m249-1.pep	KNALP	DAVAIH	YAVCKD	SSGDA	PTLS	DSGAFSSNCDNKANGDT
g249						
	180	190	200			
m249-1.pep	RTN	LEVSG	DNIV	YTYQ	ARV	GGREX
g249						
	190	200				

```
>gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas aeruginosa]
>gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader sequence [Pseudomonas aeruginosa]
>gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185
Score = 50.4 bits (118), Expect = 9e-06
Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)
```

Query: 13 QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQNLMEGLMNPPTI 72  
 OSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + ++ NL+E M +P

Sbjct: 12 QSGFSMIEVLVALLISIGVLGMIAMOGKTIQYTADSVERNKAAMLGSLNLLSMRASPKA 71

Query: 73 DSDSNKKNYNLYMGNNHALSVVDGDFQVDAIKTKTQLAEA---QLKRFSYELKNALPDAA 129

576

D + M G A + T L +A +L ++ ++KN LP A  
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAPPTAPSSCTPLPDAIKDRLGCGWAEQVKNELPGAG 126  
 Query: 130 AI---HYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTL-IKVLWVNDASAGDSDIARTNL 185  
 + Y +C+ S +CDG G L I++ W + A ++  
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLERLAWRGKQGACVNAADSSA 172  
 Query: 186 ETN 188  
 +T+  
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	NPQSG	MALIE	VLVAM	LVLTIG
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLM	EGLMN	PTID	SDSN	KKNYN	LYMGNH
a249	NLM	EGLMN	PTID	SDSN	KKNYN	LYMGNH
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKN	ALPD	AAAI	HYAV	CKDSS	GNAPT
a249	LKN	ALPD	AAAI	HYAV	CKDSS	GNAPT
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRT	NLEV	SGDN	IVYTY	QARV	GGREX
a249	ART	NLET	NGNN	IVYTY	QARV	GGREX
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcaggcgcg gcaaaaaggt atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcggcatat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTASPRDE FIRIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GGCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCGGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGG
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSP LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPL ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/g250

```

              10      20      30      40      50      59
m250.pep      MHTSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTSMNFAGGSEF
              ||:::|||||||||||||||||||||||:|||||||:|||||
g250           MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF
              10      20      30      40      50      60

              60      70      80      90      100     110
m250.pep      ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRTVFYVX
              |||||||:|||||:|||||:|||||:|||||:|||||
g250           ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRAVFFV
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250.seq

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGCTA	ACCTGTGGGC
201	GGAACTCTG	CCGATACTGC	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
251	CTCGGCATAT	CTGATGGGG	G, CGGCAC TT	GCCCCGACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

a250.pep

1 MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMOGGQKG MSWLEMLLMT  
51 GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCPAPER  
101 TAEKSRRATV FYV\*

**m250/a250** 94.6% identity in 111 aa overlap

```

a250      54.8% identity in 111 aa overlap
              10              20              30              40              50
59
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTSMNFAGGSEF
              |
||:|||||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTGMNFAGGSEF
              10              20              30              40              50
60

              60              70              80              90              100             110
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVFYVX
|||||||||||||||||||||||||||||||||:|||||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRARTVFYVX
              70              80              90              100             110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

g251.seq

```

1   atgcctgacc caatagggat tcttttcgct gccgtcggg  ttgatttttt
5   tgccgttggt ttgagggggc gttttcaacg aaataggcgc gttggcatgt
101 tgataataat aatcctgatg qcggaggctc gaaccaaacc ggctcgtaacc

```

578

```

151 gaggttgacg ctcaggttgt ggcggatttt ggcggatcgc aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaaata caccggtcgc
251 gatattgtagt aggaagacgg cttgtcggca ctcgggcccgc aatatttgctc
301 cgaaccgctcg gcggaacagc gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag aggcgggcat aatccgcca agtgtcttta
401 tcggcattgg tatagacata ttccaaaccg tagcggcttt tgggtgctgcg
451 ctgctcgtaa aacacgcccg taccgtattc cgcgcccacc tccgcaccgt
501 tttcacggtt ggtaatcagc ccgctgtatt tgcggccgcc cgcgtatttg
551 ccgtagcctc ttatcgatcc gtatttttta tttcatcaa aaaccgcctt
601 ggtagcgaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcgcg
651 tgcgttcgag tatgcccgcg atgtagtgcc gtttgttttc aaaacgaaaa
701 cccggcgga acagccacga ccggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1  MPDPGILFA AVGVDFFAVV LRGFRQIRGA VGMLIIILM AEVGTKTVVT
51  EVDAQVVADF GGIEGFECRL LQEPVAFVFN HAVGVFVGRR LVGTAAIFV
101 RTVGGTVRLK KMIVQTDALP VVREAGIIRP SVFIGIGIDI FOTVAAFVGR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYRS VFFIFIKNRL
201 GQECNRNHIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1  ATGCGTGTCTG CGGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCACC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTTT CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTCACTGCCG GTTGGGGCTG ATTTTTTTGC CGTTGTTTTC AGGGGGCGTG
251 TCTGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCCGAG ATTCACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTTGA ATGCCGCCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTTGTCCGA ACCGTCGGCA GAACAGTGCG
501 TCTGCTGAAA ATGATTATCC AAACCGATGC CCTGCGGTC GTAAGAGAGG
551 CGGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAACAC ACGCCCGTAC
651 CGTATTCCGC GCCCACCAGC GCACCGTTTT CGCCGTTGGT AAACAGTCCG
701 CCGTATTTGT GGTGCCCCG GTATTGCCC GTACCGGGCA AAGAACCCGC
751 CTGTTTTTTA TTGTCATCAA AAACCGCCTT GGTGAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGAAAA GTTTGTTGCG TGTGTTGAG TATGCCGCCG
851 ATGTAGTGCC GCTTATTCTC AAAACGAAAA CCCGGGCGGA ACAGCCACGA
901 CCGGCTTTTC TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1  MRAAVVQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51  LPRNDISPAY GDPGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIILMA
101 EIRAKAVKPE IHAQVVADFG GIEGFECLRL QEPVAFVFNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFVRL VVKHARTVFR AHQRTVFAVG QSAVFPVVAR VFAVTGQTR
251 LFFICIKNRL GQECNRNHIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40      50      60      70      80      90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAYGDPGAGFTA VGADFFAVVL RGRVRRIGAVG
          |||| |::|:|||||:|:|:|
g251      MPDPGILFAAVGVDFFAVVLRGRFRQIRGAVG
          10      20      30

```

```

                100      110      120      130      140      150
m251.pep    MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFPECRLQEPVAFPNHAGFVIGKRLV
              |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g251        MLIIIIILMAEVGKTQVTVTEVDAQVVADFGGIEGFECRLQEPVAFPNHAVGVFVGRRLV
              40       50       60       70       80       90

                160      170      180      190      200      210
m251.pep    GTRAAIFVRTVGRTVRLLKMIIQTALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g251        GTRAAIFVRTVGGTIVRLLKMIVQTALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV
              100      110      120      130      140      150

                220      230      240      250      260      270
m251.pep    VKHARTVFRAHQRTVFAVGKQSASFVVVARVFAVTGQRTLFFICIKNRLGQECRNRHIAR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g251        VKHARTVFRAHLRTVFTVGNQPAVFFAAARVFAVASYRS-VFFIFIKNRLGQECRNRHIAR
              160      170      180      190      200      210

                280      290      300
m251.pep    VESLLRVFEYAADVVPPLILKTKTRAEQPRPAFVX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g251        VESLLRAFEYAADVVPVFVKTKTRAEQPRPAFVX
              220      230      240

```

```
a251.seq
1  ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCACC
51  TGCCCAACAG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTGCCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACCCAATTC CCTGCCTAT GGTGACCCAA TAGGGTTAGT
201 CCTTGCCGCC TTGGGGGTTG CGGGTTTTAG GGGGCGTTTT CGACGAATGT
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCGAGAT TCACGCTCAG GTTG TGCGCG ATTTTGCGCG
351 TATCGAAGGA TTTTGTGAAT GCCGCTGCA AGAGCGTGTG GCTTCCCCG
401 TAAATCACGC GGTCCGATTT TGTAGTAGAA AACGCCTGTG CGGCATTCGG
451 GCGCAATAT TTGTCGGAAC CGTCCGCAGA ACAGTGCCTC TGCTGAAAAT
501 GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGCGG GGCATAATCC
551 ACCCAAGTGT CTTTATCGGC ATTGGTATAG ACATATTCCA AACCGTAGCG
601 GCCTTTGGTG TGCCTCTCGT CGTAAACAC CCGCGTACC TCGTCCGCG
651 CCACGAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701 TCGCCCGCGT ATTTGCCGTT GCCTCTTATC GGTCCGTATT TTCTATTTTC
751 ATCAAAAACC GCCTTGTGTA GGAATGCCGG AACCCTATA TCGCGCGTGT
801 CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCGGATGTA GTGCGCGTTG
851 TTTTCAAAAC GAAAACCCGG CGGGAACAGC CACGATCGGC TTTCTGATGA
```

```
a251.pep
1  MRAAVVVAQP RADIRPPAQT DIVPNCRVIA FAVDAARRAV RISIVAQAAD
51  LPRNHISPAY ADPIGLVLAA VGVGGFGRGF RRGAVGMLI IITLMAEIRV
101 KAVKTEIHAQ VVADFGGIEG FFECRLQEPV AFFVNHAVGF VVGKRLVGTR
151 AAIFVRTVGR TVRLLKMIVQ TDALPVVREA GIHPVSVFGE IGIDIFQTVL
201 AFGVLRLVKH ARTVFRAHQR TVFAVGKQTA VEVVARFEAV ASYRSVSFIF
251 IKNRLGQECR NRHRIAVESL LRVFEYAADV VPFVFKTKTR AEQPSAFV*
```

```

a251      88.5% identity with a251
              10          20          30          40          50          60
m251.pep  MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a251      MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY
              10          20          30          40          50          60

              70          80          90         100         110         120
m251.pep  GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVADFG
          :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||

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a251      ADPIGLVLAAVGVGGF----RGRFRRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVADFG
              70              80              90              100             110

              130             140             150             160             170             180
m251.pep  GIEGFFECRLQEPVAFPNHAIGFVIGKRLVGTRAAIFVRTVGRTVRLKMIQTDALPV
            |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a251      GIEGFFECRLQEPVAFPNHAVGVVIGKRLVGTRAAIFVRTVGRTVRLKMIQTDALPV
              120             130             140             150             160             170

              190             200             210             220             230             240
m251.pep  VREAGIIRPSVFIGIGIDIFQTVAAGFVRLVVKHARTVFAHQRTVFVAVGKQSAVFVVAR
            |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a251      VREAGIIRPSVFIGIGIDIFQTVAAGFVRLVVKHARTVFAHQRTVFVAVGKQTAVFVVAR
              180             190             200             210             220             230

              250             260             270             280             290             300
m251.pep  VFAVTGQTRLFFCIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR
            ||||:|:|:|:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a251      VFAVASYSR-VFSIFIKNRLGQECRNRIARVESLLRVFEYAADVPLVFKTKTRAEQPR
              240             250             260             270             280             290

m251.pep  PAFVX
            ||||
a251      SAFVX
            300

```

g253.seq

g253.pcp

1 MIDRDRMLRD TLERVAGSF WLWVVASMM FTAGFSGTYL LMDNQGLNFF  
51 LVLLAGVLGMN TLMLAVWLAT LFLRVKVGRF FSSPATWFRG KGPVNQAVLR  
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSVLLLLLV RQYTFNWEST  
151 LLSNAASVRA VEMLAWLPK LGFPVPDARA VIEGRNGNT ADARASGGLL  
201 VGSIVCYGIL PRLLAVVCK ILKLTSENGL DLEKTYQAV IRNRWQKITD  
251 ADSRRETVSA VSPKIVLND PKWALMLETE WQDQWFEGR LAQEWLDKGV

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

seq	1	ATGATTGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
51	GGGGTCGTTT	TGGTTGTGGG	TGGTGGCGGC	GACGTTTGCA	TTTTTTACCG	
101	GTTTTTCAGT	CACCTTCTTT	CTAATGGACA	ATCAGGGTCT	GAATTTCCTT	
151	TGGGTTTTTG	CGGCGTATGT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG	
201	GTTGGCAATG	TGTGTTCTGC	GTGTGAAAGT	GGGGCGTTTT	TTCAGCAGTG	
251	CGGCGACGTG	GTTTCGGGGC	AAAGACCCTG	TAAATCAGGC	GGTGTGCGG	
301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTTGA	AAATAGCGCG	
351	AACGTCGCAC	AGCCTGTGGC	TCTGCACGCT	GCTCGGAATG	CTGGTGTCCG	
401	TATTGTTGCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAGACGAC	
451	CTGTTTGAGCA	ATGCCGCTTC	GCGACGCGCG	GTGGAATGTG	TGGCATGGCT	
501	GCCGTCGAAA	CTCGGTTTCC	CTGTCCCCGA	TGCGCGGGCG	GTCATCGAAG	
551	GCCGTCTGAA	CGGCAATATT	GCCGATGCGC	GGGCTTGCTG	GGGGCTGGGT	
601	GTCCGCGAGTA	TCCCGCTGTA	CGGCATCCGT	CCGCGCTCTC	TGGCTTGGGT	
651	AGTGTTGATA	ATCCTTTTGA	AAACAAGCGA	AAACGGATTG	GATTTTGGAAA	
701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCAGT	
751	GCGGATACGC	GTCGGGAAAC	CGTGTCCGCC	GTTTCACCGA	AAATCATCTT	
801	GAACGATGCG	CCGAAATGGG	CGGTATGCTG	GGAGACCGAG	TGGCAGGACG	
851	GCGAATGGTT	CGGAGGCAGG	CTGGCGCAGT	AATGGCTGGA	TGAAGGCGTT	
901	GCCACCAATC	GGGACACAGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA	
951	ACCGGCGCAA	CTGCTTATCG	GCGTGCGCGC	CCAAACTGTG	CCGGACCGCG	
1001	GCGTGTTCGG	GCAGATGTGC	CGACTCTCGG	AAGCGGCGCA	GGGCGGCGCG	
1051	GTGGTGCAGC	TTTTGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA	
1101	GCTGGAACAT	TGGCGTAAAG	CGGTCGCGTA	ATGCGGCGCG	GCGTGCGCTG	
1151	AGCCTGCACAG	GCGGCGGCAG	GAAGGCGGTT	TGAAAGACCA	ATAA	

```

1 MIDNRNMLRE TLERVVAGSF WLWVVAATFA FFTGFSVTYL LMDNQGLNFF
51 LVLGAGVLGMN TLMLAVWLAM LFLRVKVGFR FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLLV RQYTFNWEST
151 LLSNAASVRA VELMLAWLPSK LGFPVPDARA VIEGRNLNGNI ADARAWSGLL
201 VGSIACYGIL PRLLAWVVK ILLKTSENGL DLEKPPYYAQ IRRWQNKITD
251 ADTRRETQVA VSPIKIILDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 ATNRKEQVAAL ETELKQKPAQ LILIGVRAQT PDRGVLRRQIV RLSEAAQGGGA
351 VQLLAEQGL SDDLSEKLEH WRNALAECGA AWLEPDRAAQ EGRLKQD*

```

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLVVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	:    :       : :: :					
g253	MIDRDRLRDLTLEVRAGSFWLVVVASMMFTAGFSGTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	:     :     :     :     :					
g253	TLMLAVWLATLFLRVKVGRRFFSSPATWFRGKGPVNQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVQRYYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	:     :     :     :     :					
g253	SLWLCTLLGMLVSVLLLLLVQRYYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180



582

	190	200	210	220	230	240
m253 . pep	VIEGR	LN	GN	IA	DAR	AW
g253	VIEGR	LN	GN	IA	DAR	AW
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRR	WQ	NK	IT	DA	DR
g253	IRR	WQ	NK	IT	DA	DR
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATN	RE	QV	AA	LE	TE
g253	AAN	RE	QV	AA	LE	TE
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDD	LSE	KLE	HWR	NAL	AE
g253	SDD	LSE	KLE	HWR	NAL	TE
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253.seq
1  ATGATCGACA  GGAACCGTAT  GCTGCGGGAG  ACGTTGGAAC  GTGTGCGTGC
51  GGGGTCGTTT  TGGTTGTGGG  TGGCGGCGGC  GACGTTTGCG  TTTTTCACCG
101  GTTTTTCAGT  TACTTATCTT  CTAATGGACA  ATCAGGGTCT  GAATTTCTTT
151  TTGGTTTGGG  CGGGCGTGTT  GGGCATGAAT  ACGCTGATGC  TGGCAGTATG
201  GTTGGCAATG  TTGTTCTGCG  GCGTGAAAGT  GGGGCGTTTT  TTCAGCAGTC
251  CGGCGACGTG  GTTTCGGGGC  AAAGACCCCTG  TCAATCAGGC  GGTGTGCGCG
301  CTGTATGCGG  ACGAGTGGCG  GCAACCTTCG  GTACGTTGGA  AAATAGGCGC
351  ACGTCGCGAC  AGCCTGTGGC  TCTGCACGCT  GCTCGGAATG  CTGGTGTGCG
401  TATTGTTGCT  GCTTTTGGTG  CGGCAATATA  CGTTCAACTG  GGAAGCACG
451  CTGTTGGGCG  ATTCGTCTTC  GGTACGGCTG  GTGGAAATGT  TGGCATGGCT
501  GCCTGCGAAA  CTGGGTTTTC  CCGTGCCTGA  TGCGCGGGCG  GTCATCGAAG
551  GTCGTCTGAA  CGGCAATATT  GCCGATGCGC  GGGCTTGCTC  GGGGCTGCTG
601  GTCGGCAGTA  TCGCCTGCTA  CGGCATCCTG  CCGCGCCTCT  TGGCTTGGGC
651  GGTATGCAAA  ATCCTTTTGA  AAACAAGCGA  AAACGGCTTG  GATTTGGAAA
701  AGCCCTATTA  TCAGGCGGTC  ATCCGCCGCT  GGCAGAACAA  AATCACCAGT
751  GCGGATACGC  GTCGGGAAAC  CGTGTCGCC  GTTTCGCCGA  AAATCGTCTT
801  GAACGATGCG  CCGAAATGGG  CGGTCATGCT  GGAGACCGAA  TGGCAGGACG
851  GCGAATGGTT  CGAGGGCAGG  CTGGCGCAGG  AATGGCTGGA  TAAGGGCGTT
901  GCCGCCAATC  GGGAACAGGT  TGCCGCGCTG  GAGACAGAGC  TGAAGCAGAA
951  ACCGGCGCAA  CTGCTTATCG  GCGTGCGCGC  CCAACTGTG  CCCGACCGCG
1001  GCGTGTTGCG  GCAGATCGTC  CGACTTTCGG  AAGCGGCGCA  GGGCGGCGCG
1051  GTGGTGCAGC  TTTTGGCGGA  ACAGGGGCTT  TCAGACGACC  TTTTCGGAAA
1101  GCTGGAACAT  TGGCGTAACG  CGCTGACCGA  ATGCGGCGCG  GCGTGGCTGG
1151  AACCCGACAG  AGCGGCGCAG  GAAGCCGCTC  TGAAAACCAA  CGACCGCACT
1201  TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253. pep
1  MIDRNRMLRE  TLERVRAGSF  WLWVAATFA  FFTGFSVTYL  LMDNQGLNFF
51  LVLAVGLGMN  TLMLAVLAM  LFLRVKGRF  FSSPATWFRG  KDPVNQAVLR
101  LYADEWRQPS  VRWKIGATSH  SLWLCTLLGM  LVSLLLLLV  RQYTFNWEST
151  LLGDSSSVRL  VEMLAWLPK  LGFPVPDARA  VIEGRNLNGN  ADARAWSGLL
201  VGSIACYGIL  PRLLAWVCK  ILLKTSENGL  DLEKPYQAV  IRRWQNKITD
251  ADTRRETQSA  VSPKIVLND  PKWAVMLETE  WQDGEWFEGR  LAQEWLDKGV
301  AANREQVAAL  ETELKQKPAQ  LLIGVRAQTV  PDRGVLRQIV  RLSEAAQGGG
351  VVQLLAEQGL  SDDLSEKLEH  WRNALTECGA  AWLEPDRAAQ  EGRLKTNDR
401  *

```

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFVLVLAGVLGMN					
a253	MIDRNRMLRETLEVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFVLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFRLVKVGRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFRLVKVGRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLSNAASVRAVELMAWLP SKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIA CYGILPRLLAWVCKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIA CYGILPRLLAWVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRET VSAVSPKIILNDAPKWAVMLETEWQDGEWFEGR LAQEWLDKGV					
a253	IRRWQNKITDADTRRET VSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGR LAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVA ALET ELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVA ALET ELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGR LK DQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGR LK TNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg tttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggccgggc
301 tggacgggat tttcactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggctcttg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence &lt;SEQ ID 994; ORF 254.ng&gt;:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG  
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYVMGW MVLAVMKSLT  
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF  
 201 VSVYGYVI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)  
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTGA GTTCCTGGCT  
 51 GTACCACGGA ATTGCAGCCG GAAAACTGAA AAGCATTGTG AAAAAACCG  
 101 ACCACTGCAT GATTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA  
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG  
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA  
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATT ATGTCGTCAT GGGTTGGATG  
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT  
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTGGC ATTACTGGT  
 401 TTGTAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTT  
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGTGACG GTTACGTAAT  
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)  
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI LKKTDHCMYI VLIAGSYTPFA  
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IYIYVMGWM  
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF  
 151 VLGGSITQFV SVYGYVI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng)

from *N. gonorrhoeae*:

m254/g254

				10	20	30
m254.pep				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGLMLMLLKTIGHGDGYRIFSVSVYGISLLL	LYLSSSLYHG	IAAGKLKSI			
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAAGIAQELT
g254		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAAGIAQELT
		80	90	100	110	120
m254.pep		100	110	120	130	140
		IYIYVMGWM	MVLAVMKSLT	ASLPSAGLAW	LAAGGMLYSV	GIYWFVNDEK
g254		IYIYVMGWM	MVLAVMKSLT	ASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK
		140	150	160	170	180
m254.pep		160				
		VLGGSITQFV	SVYGYVIX			
g254		VLGGSITQFV	SVYGYVIX			
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq  
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGTA GCGGTTTGAT  
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG  
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT  
 151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAACCT  
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG  
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGCGCGGGC

301 TGGACGGTAT TTTCAC TGTC CTGGCTGCTG GCGGCTGCAG GAATCGCACA  
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA  
401 TTTATATCGT AATGGGCTGG ATGCTCTTGG CGGTAATGAA ATCCCTGACA  
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT  
501 GTACAGCGTC GGCATTTACT GGTTTGTAA CGATGAAAA ATCCGACAG  
551 GGCACGGAAT CTGGCATCTG TTCGTATTGG GCGCGACGAT CACCCAATTT  
601 GTCACGCGTGT ACGGTTACGT AATCTGA

a254.pep

1 MYTGERFNTY SHLSGLILAA AGLALMLLKT<sup>+</sup>IGHGDGYRIF SVSVYGISLL  
51 LLYLSSSLYH GIAAGLKLSI LKKTDHCMIIY VLIAGSYTPF ALVSLRNGPG  
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIATYIVMGL MVLAVMKSLT  
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRRHGHIWHL FVLGGSITQF  
201 VSVYGYVI\*

10 20

```

30
m254.pep
VSVYGISLLLLYLSSWLYHGIAAGKLKSIL
|||||
|||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLYLSSSLYHGIAAGKLKSIL
20 30 40 50 60
70
40 50 60 70 80
90
m254.pep
KKTDHDCMIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHDCMIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
80 90 100 110 120
130
100 110 120 130 140
150
m254.pep
IVIYVVMGWMVLAVMKSILTASLPSAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
|:|:|
|||||
a254
IAIYIVMGWMVLAVMKSILTASLPPAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
140 150 160 170 180
190
160
m254.pep
VLGGSITQFVSVYGYVIX
|||||
a254
VLGGSITQFVSVYGYVIX
200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

Seq					
1	atggttggaac	aggaagcctt	gcggggtcag	ttcgtcgccg	tgttcgctgc
51	cgcgttgctg	tacgttgtca	aaacctgcgc	cgatttccac	gcctttgacg
101	gcgttgatgc	ccatcatcgc	gtaggcgatt	tcggcatcga	ggcggctgaa
151	aacgggttcg	ccccaaccca	cggggacgtt	ggcggttcg	atatgcagt
201	tcgcgccgac	ggaatccaag	gatttgcgca	caccgtccat	tattgtttcc
251	agttcggcga	tttgacttgg	gttggcgcca	aaaaaaggat	tttgggaaat
301	gtgttcgctg	ccttcaaacc	ggattttttt	ttcgccgact	tgggtaacgt
351	aggcggtgat	ttcgtgccc	aatttttctt	tcagccattt	tttggcaacg
401	gctccggcgg	caacgcgggc	tgcggtttcg	cgggcggaac	tcttgccgc
451	gccccggtag	tcgagcggtac	cgtatttgtg	ccaataggta	tagtcggcgt
501	gtccggggcg	gcagcggttg	gcgatgtcgc	cgtagtcttc	gctgcgctgg
551	tcgggttgct	ggattggt			

g255.pcp

1 MVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAHHR VGDFGIEAVE  
51 NGFAQTGDGV GGFDMQFRAD GIQGFHAHTVH IVFQFGDLAL VGGKKRILGN  
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNSSGGNAG CGFAGGTPAA  
151 APVVARTVFV PIGIVGVSGA EGGGDVAVVF AALVGVD\*

m255.seq

Seq	1	2	3	4	5	6
1	GTGGTTGGAC	AGGAAGCCTT	GCGGGGTCAG	TTCGTCGCCG	TGTTGCGCTGC	
51	CGCGTTGCGT	TACGCTGTCA	AAACCTGCGC	CGATTTCAC	GCCTTTGACG	
101	GCGTTGATGC	CCATCATCGC	GTAGGCGATT	TCGGCATCGA	GGCGGTCAAA	
151	AACAGGTTTCG	CCCAAGCCGA	CAGGGACATT	GGCTGCTTCG	ATATGCAGCT	
201	TCGCGCCGAC	GGATTCCAAG	GATTTGCSCA	CGCTGCTCAT	ATAGTTTTC	
251	AGCTCGGCAA	TTTGGCTATG	TTTGGCGGCA	AAAAAAGGAT	TTTGGGAAAT	
301	GTGTTGCGAG	CCTTCAAACC	GGATTTCCTT	TTCGCCGACT	TGGGTAACGT	
351	AGGCGGTGAT	TTCCGTGCCG	AATTTTCTT	TCAACCATTT	TTTGGCAACG	
401	GCTCCGGCAG	CAACGCGGGC	GGCGGTTTCA	CGGGCGGAGC	TCCTGCCGCC	
451	GCCGCGGTAG	TCGCGCGTGC	CGTATTGTG	CCAATAGGTA	TAGTCGCGCT	
501	GGCCGGGGCG	GAAGCTGGTG	GCGATGTTGC	CGTAGTCTTT	GCTGCGCTGG	
551	TCGGTATTGC	GGATTAA				

m255.pcp

1 VVGQALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVK  
51 NRFAQADRLD GCFDMQLRAD GIQGFAAHAVH IVFQLGNLAM VGGKKRILGN  
101 VFAAFKPDFD FADLGNVGGD FRAEFFFQPF FGNGSGSNAG GGTGGAPAA  
151 AAVVARAVFV PIGIVGAGA EAGGDVAVF AALVGIAD\*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/g255

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVKNRFAQADRD	I	:	:	:	:
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVENGFAQTGDG	D	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFAHAVHI	VFQLGNLAMVGGKKRILGNVFAAFKPDFF	FFADLGNVGGD	:	:	:
g255	GGFDMQFRADGIQGF	FAHTVHI	VQFGDLALVGGKKRILGNVFAAFKPDFF	FFADLGNVGGD	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFFFQPF	FGNGSGSNAGGGFTGGAPAA	AAVVARAVFVPIGIVGVAGAEAGGD	VA	VF	:
g255	FRAEFFFQPF	FGNGSGGNAGCGFAGGT	PAAAPV	VARTVFVPIGIVGVSGAEGG	GD	VA

130            140            150            160            170            180

189

```
a255.seq
1 GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCGTGC
51 CGCGTTTCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGCG GTAGGCGATT TCGGCATCGA GCGCGTCGAA
151 TACGGGTTTCG CCAAGCCGA CGGGACGTT GCGCGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTTCGCGA CGCTGTCCAT ATAGTTTTCC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAGGAT TTTGGAAAT
301 GTGTTFCGAC CCTTCAACAC GGAATTTCTT TTCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTTCTT TCAACCATT TTTGGCAACG
401 GCTCCGCGCG CAACGCGGGC GCGCGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GCCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT CTGCGCTGGT
551 TCGGTATTGC GGATTAA
```

a255.pap

1	VVGQ <b>EALRGE</b>	FVAVFAAALR	YAVKTCADFH	AFDGVDAHHG	VGDFGIEAVE
51	YGFAAQADGDV	GGFNMQLRAD	GIQGF <del>AH</del> AVH	IVFQLGNLAM	VGGKKRILGN
101	VFAAFKPDFF	FADLGNVGGD	FRAE <b>FFFPF</b>	FGNGSGGNAG	GGFAGGT <b>PAA</b>
151	APVVARAVFV	PIGIVGVAGA	EAGGDVAVVF	<b>AALVGIAD*</b>	

		10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVKNRFAQADRD	I					
a255	VVGQEALRGFEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVEYGAQADGDV						
		10	20	30	40	50	60
		70	80	90	100	110	120
m255.pep	GCFFDMQLRADGIQGFAHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD						
a255	GGFNMQLRADGIQGFAHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD						
		70	80	90	100	110	120
		130	140	150	160	170	180
m255.pep	FRAEFFQPFNGSGSNAGGGFTGGAPAAAAVVARAVFVFIGIVGVAGAEAGGDVAVVF						
a255	FRAEFFQPFNGSGGNAGGGFAGGTPAAAPVVARAVFVFIGIVGVAGAEAGGDVAVVF						
		130	140	150	160	170	180
		189					
m255.pep	AALVGIADXX						
a255	AALVGIADXX						

```
g256.seq
1 atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcctg
51 cagctgcggc ggcgtagcga acaccgcccc ggtgttctac cacttgggttg
101 ataccgcgga aatcgccctt gctttggaca cgctcacccg cggttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttggggcga cagggcaaaa aggcattgcc gcacgcttcg cgcgcgcatc
251 ccgccccctg tgatgcagag gcggcagcca gccgcttcga cagcggcgatc
301 accgcggtgc tctacacgcg ctacttcttc cgcacactga tacccaaagc
```

588

```

351 acgttcgctc caagggtttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcagcact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgcccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgcgggcttt gtcagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701 tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

g256.pep

```

1 MLAVRNRGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
51 EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

m256.seq

```

1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGTAGTCG TCCATTTCCG
51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTATCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTT AGACGGCATT TGCCGAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCTGTTC
601 CAGCCGGCAT ATGGTGGTCA TGTGGGCTTT GTCAGCAGCA CCGCGGCGAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

m256.pep

```

1 MLAVRDRGWH GVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFARYR
51 EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPAYGGHVG FVSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	:     :     :     :     :     :     :     :     :					
g256	MLAVRNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAAVISAPVDAEAAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	:     :     :     :     :     :     :     :					
g256	GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAAGSRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCKPLLKHVAKPLLLLNNAVNDP					
	:     :     :     :     :     :     :     :					
g256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCKPLLKHVAKPLLLLNNAANDP					

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```

a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCGG
51  CAGCTGCGGC GCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACGCGCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGCGGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCACTC
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG TACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCTGCG AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCCTGTTT
601 CAGCCGACAC ACGGTGGTCA TGTCGGCTTT GTCGCGACGA CCGCGCGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCTAT TTCGACAGCT
701 TCCGCACAAA CAGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```

a256.pep
1  MLAVDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIYAVGVS LG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVGSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVDRGWHGVVHFRSCGGIANTAPVFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	:     :     :     :     :					
a256	MLAVDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGGKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	:     :     :     :     :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	:     :     :     :     :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```

g256-1.seq
1  ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGCGACCC GCATACCGCC

```



```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTCCGC CGATGCGCCG CTGGTCGTGC TGTTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGGAAGTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GCGCGAGTCG TCCATTTCCG CAGCTGCGGC
301 GCGGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCGCCGTAT CCGCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGTGTC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAAACAGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 GCCCCGTGCA GACGAAGCGT CCGAAGCCGT TACCTGTTC CAACCTGCAC
851 ACGCGGGGCA CGCCGGCTTT GTCAGCAGCA CCGCGGCGAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTAT TTTGACAGT TCCGCACAAA
951 CAGCGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVRNRGWH GAVVHFRSCG
101 GVANTAPVFY HLGDTAEIAF ALDTLTARYR EYAVGVSLG GNAPAKYLGE
151 QGKRALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFD RHDYYRQTSK PLLKHVAKP
251 LLLNNAANDP FLPPEALPRA DEASEAVTLF QPAHGGHAGF VSTGGRLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCAGCGCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCCGCCGA TGCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAAGTATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTCCGCAG CTGCGCGGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACAC TTTGGCGATA CCGCCGAAT
351 CGCCTTTACT TTGGACAGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGCGCGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAGAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAG CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCG ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCGAGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVDRGWGH VVHFRSCGG
101 IANTAPVFYH LGDTAEIAFT LDTFAARYR EYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFD RHDYYRQTSK PLLKHVAKPL
251 LLLNAVNDP FLPEALPRAD EVSEAVTLFQ PAYGQHVGFV SSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRRELLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWGVVHFRSCGGIANTAPVFYHLGDTAEIAF

```

591

```

g256-1  |||||
LVVLFHGLEGSSRSHYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
          70      80      90      100     110     120

m256-1.pep 120      130      140      150      160      170      179
TLDTFAARYREIYAVGVS LGGNALAKYLGEQGGKALPQAAVISAPVDAEAGRRFDSGI
g256-1  |||||
ALDTLTARYREIYAVGVS LGGNAPAKYLGEQGGKALPHASAAVSAPVDAEAGSRFDSGI
          130      140      150      160      170      180

m256-1.pep 180      190      200      210      220      230      239
TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFETAPLHGFADRHDYYRQTSC
g256-1  |||||
TRLLYTRYFLRTLIPKARS LQGFQTAFAAGCKTLGEFDDRFETAPLHGFADRHDYYRQTSC
          190      200      210      220      230      240

m256-1.pep 240      250      260      270      280      290      299
KPLLKHVAKPLLLLNAVNDFLPPEALPRADEVSEAVTLFQPAYGGHVGVFSSTGGRLHL
g256-1  |||||
KPLLKHVAKPLLLLNAANDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSSTGGRLHL
          250      260      270      280      290      300

m256-1.pep 300      310      319
QWLPQTVLSYFDSFRTNRRX
g256-1  |||||
QWLPQTVLSYFDSFRTNRRX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1..seq
1  ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCGCCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCGCTG GTCTGCTGT TTCACGGTTT
201 GAGGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCA TGGGCGGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAATATTT GGGCGAACAG
451 GCGCAAAACG CGCTGCCGCA AGCCGCCGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACAGCGCCTA CTTCCTCCGC ACACTGATAC CAAAGCAGC GTCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAACC TTCTTGCAAA CCGCTGCTCA AACACGTTGC CAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCGG AAGCCGTTAC CCTGTTCAG CCGACACAG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG CGGCGAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1..pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVS LGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDFP LPPEALPRAD EVSEAVTLFQ PTHGGHVGVFV GSTGGRLLHQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

          10      20      30      40      50      60
a256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
m256-1  |||||
MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

          70      80      90      100     110     120
a256-1.pep VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVVHFRSCGGVANTAPVFYHLGDTAEIAFT
m256-1  |||||
VVLFHGLEGSSRSHYAVELMLAVDRGWNGVVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAVISAPVDAEAAGNRFDSGIT					
m256-1	LDTFAARYREIYAVGVSLGGNALAKYLGEQGKKALPQAAVISAPVDAEAAGRRFDSGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAGCKTLGEFDDRFTAPLHGFAADRHYYRQTSCK					
m256-1	RLLYTRYFLRTLIPKAKSLQGFQTAFAGCKTLGEFDDRFTAPLHGFAADRHYYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNAVNDFLPPEALPRADEVSEAVTLFQPTHGGHVGFGSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNAVNDFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

```

g257.seq
1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcgggtt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgag atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgagg ctgcgcctgt tcggcggtgga
201 cgacagacag gcggcggatt tggccaataa ggttttggcg gaagtggcgc
251 gtttgaaaaa aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaaccgag acggttatct gacttcgcct ccggcggatt ttttggaaact
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

```

g257.pep
1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMF5 LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

```

m257.seq
1  ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGAC. GCGGCgGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCT CACTGGGTTC CGGTGCGGa. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATGTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAAC
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

```

m257.pep
1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRNVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKLVA EVARLEKLF5 LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60

593

```

m257.pep  MGRHFGRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAD
          |||||:||||:||||: ||||| ||||| :||:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

## a257.seq

```

1  ATGGGCAGGC ATTCGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
51  GCGGCGGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAATAAAGAT GAAAAACGCA ATGAAAATGT GTTTTCTG
151 AAAGGTGTCG CACTGGGTTC CGGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA AATGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGT
301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAACT
351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

## a257.pep

```

1  MGRHFGRRRF LTVAAVAAG AAVSFLPNPF AADDEKRNKD EKRNVFFW
51  KGVALGSGAE LRLFGVDDRR AADLVNKKVLA EVARLEKMF SLYREDSLIS
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAX
          ||||| :|||||: |||||:|||||:
|||
a257      MGRHFGRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:
||
a257      LRLFGVDDRRRAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTX
          |||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgtgtga
51  cggattgacg gcggcgaccg gcagaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtgtt gtccgcggtt
151 ttggcacgtt atgtcatatt gctgttgaaa gacaggcgca acggcggttt
201 cggttcgtag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcccg ttcggcattt ccgcgagttt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggcggcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccgcgagcg gttttgcccc
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccgcga aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgtaa agcataggcg gcgtattgta
651 cgcgcaggga tgggtgtcgg caggtacgca caacgggcgc gattacgcgc
701 tgtttcttcg ccagccgatt ccgaaaatg tggcacagga tgcggttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc tttttcttgg taacctgtct gattgcctcg ctgctgtcga
851 tttttcttgc gctggaatg gcactgtatt ttgcccgcgg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgcccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcg ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctacccc ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLK DRRNGVFGSQ IAKRLSGMFT LVAVLPLGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKGLQOT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVDLG LTTGVVVSYP LSCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCTG TCCTGTGTGA
51  CGGACTGACG GCGGCAACCG GCAGACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TCGGTTTACG GCAATGCTGC TGCTGGTGTG GTCCGCCGTT
151 TTGGCAGGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTCTCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCGGTCGAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAAG AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCTG CGGGTACGCA CAACGGGCGC GATTACGCTT
701 TGTTTTCCG TCAGCCGTTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCTGCT GATTGCCTCG CTGCTGTGGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCGG TTTGCTGCAA
901 CCCGTCCTAT CGCTTGCCGA GGGGCGAAG GCGGTGGCGC AAGGCGATT
951 CAGCCAGACG CGCCCGTGT TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

595

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACbTT CAACAAAGCG GCGGAACAGA TTyTGGGGAT GCCGCTTACC
1201 CCCcTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAA GAAGCCGCGT
1451 GGGGCGAaGT GGCgaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGstGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCTT CGCTCAAATT GGAAATCAG GATTGAAAC CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGGTTT GCGGCGGACT
1751 TGCCGCGCAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

```

m258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSRRHWG HGVSAQSSL AEFVFAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

```

              10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAVLARYVILLLK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVSFS AMLLLVLSAVLARYVILLLK
              10      20      30      40      50      60

              70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSLNL
              70      80      90     100     110     120

              130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      SKSALDLAADNAVSNAPVQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
              130     140     150     160     170     180

              190     200     210     220     230     240
m258.pep  SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g258      SINPHQFDQPLPDKEHWEQIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI
              190     200     210     220     230     240

```

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE  ::  :                         :					
g258	PENVAQDAVLIEKARAKYAELSSYSKKGLQTFFLVTLIASLLSIFLALVMALYFARRFVE 250 260 270 280 290 300					
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTCLKFNHMTQEQLSIKEADERNRRREEAA  :					
g258	PILSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTCLKFNHMTQEQLSIKEADERNRRREEAA 310 320 330 340 350 360					
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVVFDEQGCLKTFFNKAAEQILGMPLTPLWGSSRHGWGHGVSAAQQSLL        :        : :					
g258	RHYLECVLDGLTTGVVVSYPLSCCRTAVFSTCHSSPLSYFX 370 380 390 400					

```

a258.seq
1  ATGCGCGCTT TTCTACCGAT CGCAGCCATA TGCGCCTGCG TCCTGTGTGA
51  CGGATGACG GCGGCCAACG GCAGACCAGG TTCGCTGGCG GATTATTCTT
101 GTGGGATTGT TGCCTTACAG CCAATGCTGC TGCTGTGGTT GTCCCGCTGT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCCGAG ATTGCCAAAC GCCTTTCCGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGGTTTCTG TTCGGCGTTT CCGCACAGTT TATCAACGGC
301 ACGATTAAAT CGTGTTTCGG AACAGATACC CACGAGCGCG TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATCT GCGGCAGACG AACGCCCTTG
401 GCAACGCCAT CCCCGTGCAG ATAGACCTCA TCGGCGCGCG TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC CGCGGACGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAACGGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGT CGATCAGCCG TTTCCAGGTA AGCGCGCTTG GGAAAAAATC
601 CAACAGCGCG GTTCCGTCAG GGAATTTGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CAGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGCGC TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTG CAAACCTGCT GATTGCTCGC CTGCTGTCTGA
851 TTTTCTTTC ACCTGTCATG GCGCTGTATT TCGCCCGCCG TTTGCTCGAA
901 CCCGTCTCAT CGTGTGCCGA GGAGGCGAAG CGCGTGCGCG AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCSCAACGA CGAGTTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCGGCT AGACATTATC TCGAATGCGT
1101 GTTGGAGGGG TGCACACCGG CGGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACCTT CAACAAAGCG GCGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGGTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCGCCCAT CGGCGCGCGG GCAGGTATCGG
1301 ACAAACCGGT CCATGTGAAA TATGCGCGCG CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCGAAGAC AACGGCAACG GCGTGTAAT
1401 GGTGATTGAC GACATCACC G TTTTGATACA CGCGCAAAA GAAGCGCGCT
1451 GGGGCGAAGT GGCAAAACGG CTGGCACAGC AAATCGCAA TCCGCTCAGC
1501 CCCATCCAGT TTTCTGCCGA ACGGCTGGCG TTGAAAATTGG CGGGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 AACAAAGTGG GGCATTAATA GAAATGGTCG AGGCATTCCG CAATTACGCG
1651 CGTTCCCTT CGCTCAAAT GGAATAATCG GATTGAACG CCTTAATCGG
1701 CGATGTGTTG CGATGTGTACG AAGCTGGTCC GTGCGGGTTT GCGGCGGAAC
1751 TTGCCGGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCC GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCGGA GTCAGGGTAA AATCGGAAGC GGGGCGAGAC GGACGGATTG
1901 TCTGACAGT TTGCGACAAC GGCAAGGGGT TCGCGAGGGA AATGCTGCAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGCG CGCATCAGCG
2051 TGAGCAATCA GGATGCGGGC GCGCGGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATGCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLOT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAAQSLA AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLEDE DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

m258.pep	10	20	30	40	50	60
	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVLSAV	LARYVILLK		
a258	MRRFLPIAAICAVVLLYGLTAATGSTSSLA	DYFWWIVAFS	AMLLLVLSAV	LARYVILLK		
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFL	FGVSAQFING	TINSWFGNDT	HEALERSLNL		
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFL	FGVSAQFING	TINSWFGNDT	HEALERSLNL		
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNAIPVQIDLIGAASLP	GDMGRVLEHY	AGSGFAQLAL	YNAASGKIEK		
a258	SKSALNLAADNALGNAIPVQIDLIGAASLP	GDMGRVLEHY	AGSGFAQLAL	YNAASGKIEK		
	190	200	210	220	230	240
m258.pep	SINPHKLDQPFPGKARWEKI	QQAGSVRDLE	SIGGVLYAQG	WLSAGTHNGR	DYALFFRQPV	
a258	SINPHKLDQPFPGKARWEKI	QQAGSVRDLE	SIGGVLYAQG	WLSAGTHNGR	DYALFFRQPV	
	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAE	LSYSKKGLOT	FFLATLLIAS	LLSIFLALVM	ALYFARRFVE	
a258	PKGVAEDAVLIEKARAKYAE	LSYSKKGLOT	FFLATLLIAS	LLSIFLALVM	ALYFARRFVE	
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQT	RPVLRNDEFG	RLTKLFNHMT	EQLSIAKEAD	ERNRRREEAA	
a258	PVLSLAEGAKAVAQGDFSQT	RPVLRNDEFG	RLTKLFNHMT	EQLSIAKEAD	ERNRRREEAA	
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKA	AEQILGMPLT	PLWGSSRHGW	HGVSAAQSLA	
a258	RHYLECVLEGLTTGVVVFDE	QGCLKTFNKA	AEQILGMPLT	PLWGSSRHGW	HGVSAAQSLA	
	430	440	450	460	470	480
m258.pep	AEVFAAIGAAAGTDKPVHVK	YAAPDDAKIL	LGKATVLPED	NGNGVVMVID	DITVLIHAQK	
a258	AEVFAAIGAAAGTDKPVHVK	YAAPDDAKIL	LGKATVLPED	NGNGVVMVID	DITVLIHAQK	



598

	430	440	450	460	470	480
m258.pep	490	500	510	520	530	540
	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTI IKQVAALK					
	490	500	510	520	530	540
m258.pep	550	560	570	580	589	
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIKFNAEEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

```

g259.seq
1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  ttgatttttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgcccgc
151 gcgctggtgt ggcctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatatacc
251 ccgtcctgca cgttcttttg caacacttgg aacacaagcc gcaaatgctc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgcacg attgccgcgc
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctc
451 ggcgaaacct atgggcccgt gtccgccgat attttcgagt tgcggcgccg
501 tttggaaagg cgcgcgttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

```

g259.pep
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

```

m259.seq (partial)
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTTT TTTGACCGC GCAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCTCTTTG CAACACTTGG AACACAAGCC GCAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTGCGCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

```

m259.pep (partial)
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSXALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG  
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSXALEGRAFKGMLMLKT					
g259	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALERRAFKGILMLKT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCCLPFGNGVGVGRTQSGVAGDFKNIR					
g259	AEYKXHLRRCCLPFGNGVGVGFRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTGCGCGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGCCGCGATT GTCCGCGGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGTCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAAGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAA.CATCT TCGGCGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCGCTCAAT CAGGCGTTGC AGGAGATTTC AAAAACATCG GAAAAGTCCA
651  A

```

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSVA
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDVAS
151 GETYGRVFAD IFELSALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
201 RAQSGVAGDF KNIGKVQ

```

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					

600

	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKIFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
a259	SARSKAKAEKIFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVVFADIFELSALEGRAFKGMLKLT					
a259	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVVFADIFELSALEGRAFKGMLKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRLPFGNGVGVGRVTSQSGVAGDFKNIR					
a259	AEYKXHLRRLPFGNGVGVGRAQSGVAGDFKNIGKVQ					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GCGCAAACTT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDASAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GCGCAAACTT ATGGACCGGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTTCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC AAAAACTCG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDASAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

```

      10      20      30      40      50      60
g259-1.pep  MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            |||
m259-1      MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            10      20      30      40      50      60

      70      80      90      100     110     120
g259-1.pep  SVRSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGM AEQVRFKAE
            |::|
m259-1      SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGM AEQVRFKAE
            70      80      90      100     110     120

      130     140     150     160     169 ...
g259-1.pep  VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALE
            |||
m259-1      VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT
            130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

```

a259-1.seq
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTGACCGC GCAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTC TGTCCGCATT GTCGCGCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTCGTG TCGGCGCGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACCC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAATGCTC
301 GCCCTGTGCG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCCGCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG CGCGAATATA
551 AAAACATCTT CGCGCATGCC TGCCGTTCCG AAACGCGCTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC A AACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

```

a259-1.pep
1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTD AVAS
151 GETYGRVFAD IFELSAALEG RAFKGLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

```

      10      20      30      40      50      60
a259-1.pep  MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            |||
m259-1      MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV
            10      20      30      40      50      60

      70      80      90      100     110     120
a259-1.pep  SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGM AEQVRFKAE
            |||
m259-1      SARSKAKAEK FYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGM AEQVRFKAE
            70      80      90      100     110     120

      130     140     150     160     170     180
a259-1.pep  VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT
            |||
m259-1      VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALEGRAFGMLKLT
            130     140     150     160     170     180

      190     200     210     220
a259-1.pep  AEYKNIFGDACRSETALELGALNQLQEISK TSEKSKRIFYX
            |||
m259-1      AEYKNIFGDACRSETALELGALNQLQEISK TSEKSKRIFYX
            190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

```

1  MGAGVVFVVF QPFFSLFRAL FEGGVGIVEG AHDAECDFL SEEFTRIRIG
51 RVFIDSVGQI TARFFQAFG NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGGNTVSG HFLIRTD FDD GDAVCLFQAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

m260.seq

```

seq
1  ATGGGTGCGG  GTATGGTATT  CGTTGTCTTT  CGGCCGTTCT  CCAGCCTGTT
51  TCGAGCGTTG  TTCAGGACA   GAGTCGGTAT  AGTCAGGGA   GCGCACGATG
101 CGCTGAATG   CGACTTCCTG  CCCGAGGAAT  TTACCCGTAT  CCGGATCGGT
151 GATGTTTTTA  TTGATTCGGT  AGGTCAGGTA  GCGCCCCGCG  TCTTTCAGGC
201 CTTTGGTGTA  AACCCTGGTG  CCTTGGTGT   ACAGCAGCCT  GCCTTCCGGG
251 CCCGAGwCA   sCGCGCGyGC  GGCAGCGGTT  TCTTTGCGGG  AAACGATTTG
301 CGGATGCCCG  ATAAAGATGC  GGTAGAAGTT  GACATCGATG  GCGGGAATAC
351 CGTATCCGGA  CACTTCCTTA  TCCGCACTCA  TTTTGACGAC  GGGGATGCCG
401 TCTGTCTGTT  CCAAGCCGAG  CGGCGCTTCG  CCGTCAACGT  GGCGAACAC
451 CAATACCTGG  TCCGGATAAA  TCAGGTGCGG  ATTGTGGATT  TGATCCCGGT
501 TCGCGTyCCA  CAG

```

m260.pap

```

1  MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51  RVFIDSVGQV AARLFQAFG NPGAFGVQOP AFRARXXARX GSGFFAGNDL
101 DMPHKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m260/g260

[illegible]

603

g260            GICPKYPTGCRPV  
                 190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
1   ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGTT TCTTTGCGGG AAACGATTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCT CCGTCAACGT GCGGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGGTGT CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
1   MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAAECDLFPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAAECDLFPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQLVLRINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQLVQINQVGIVDLIPVRVPPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
1   atggagcttg ggcatacgt attccttggtg ctttgcgcg gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctccggcatt cgcggcagcc gccgacgata ccctttagc aggtgtgggt
151 ctggttcgcg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgctt ggtcaggtag atcagcgcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcacg gatttgacga acacgccgcg
301 gcagtcggga tagcccgaaa aatcgggttc gcacacgcc cgcgatgatg
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgctgtgt cggcggtttc
451 gatggcgcg gtttcgatgg cggcggtttc gtccatcagg cgttgtgagc
501 taatctgccg catcaggctc aaatcgagta cgtttgact gacacccaaa
551 tcctgcgca tccactctgc gcgttcagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttgattg
```

604

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag  
701 gcttttttgggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG  
51 LFADVVQHAH FVRQRPRRLR LQVHQRRVDL KIVVHRQIKG NVHGFDEHAA  
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF  
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP  
201 VSEGDLDFV APVGLDCLNQ AGGRILTARE DDQGLV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG  
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTTCGCG CAAGATACAG  
101 CTCGGGCATT CGCGgCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT  
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCCACG  
201 TTTGCGCCTT GGTCAATAC ATCAGCGGCG TGTGGATTGT AAAATCATAG  
251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTTGACAA ACACGTCGCG  
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT  
351 CCGGTATCCC CTGCCCTTTG GCGTAAATCG CCGCATAGAG CAGGAAAAGC  
401 gCGTTGCGGC CGTCTACAAA GGTATTGCGA ACGCCGTTTT CGGCAGTTTC  
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA  
501 GgCTcAAGTC GAGTACGGTT TGTTCGACG CCAATCCTG CGCAATCCAG  
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT  
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG  
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1 MELGHIVFLM VCACSDGLFT FOIFRQPAFA QDTARAFAAA ADDAVIAGVG  
51 LLADIVQHAH FVRQRPRRLR LQIHQRRVDL KIIVHRQIKG NVHRFDKHVA  
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF  
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFOLD GMALPVLESN  
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGL LV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng)

from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	: :					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVVQHAH					
	10 20 30 40 50 60					
	70	80	90	100	110	120
m261.pep	FVRQRPRRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
	: :					
g261	FVRQRPRRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGFAHARDDVPDT					
	70 80 90 100 110 120					
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV----VHQGIVRNLPHQAVQVEYGLF					
	: :        : :          : :					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130 140 150 160 170 180					
	180	190	200	210	220	230
m261.pep	DAQILRNPAFTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
	: : :  : :					
g261	DTQILRDPLCAFQLDGMALPVSEGDLDFAPVGLDCLNQAGGRILTAREDDQGLVX					
	190 200 210 220 230					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCCTTATG GTTTGC GCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCCAAG
201 TTTGCGCCTT GGTCAAGATC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTGCGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTGACGCG CCAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	10	20	30	40	50	60
m261.pep	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	FAHARDDVPYP			
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHGFDKHVT	AVGIAGEVGF	FAHARDDVPYP			
	70	80	90	100	110	120
m261.pep	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHGFDKHVT	AVGIAGEVGF	FAHARDDVPYP			
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHGFDKHVT	AVGIAGEVGF	FAHARDDVPYP			
	70	80	90	100	110	120
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV	EYGLFDAQIL			
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV	EYGLFDAQIL			
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV	EYGLFDAQIL			
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV	EYGLFDAQIL			
	130	140	150	160	170	180
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcaa
51  accgcgcta gagcggtac ccaaaaacaa cggtttatc cccaacctca
101 tcggcgatt ggcaaacgcc ccgaagctt tggcgttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcgaag tcgaagtgat
201 ccgatcatc gccgtccgca ccaaccaatg cagctctgc gtggcagggc
251 acaccaaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgcccgcg ctttggcggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```



g263 . pep

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV  
51 GKLNAAANSLT AGEVEVIRII AVR TNQCSCF VAGHTKLATL KKL LSEQSLN  
101 AARALAAKGS DDAKLGALAA FTQAVMAKKG AVSDDELNAF LEAGYNRQQA  
151 VEVVMGVALA TLCNYANNLA QTEINPKLOA YA\*

m263.seq (partial)

```

seq      (partial)
1      ..CGACGAGCGC AATTTGACGA TGCCAAACTC GGCGCCTCG CCGCCTTCAC
51      CCAAGCCGTA ATGGCGAAAA AAGCGCGCGT ATCCGACGAG GAACTCAAAG
101     CATTTTTCGA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151     GGCAT.AsyC TgGCAACCTT GTGCAACTAC GTCAACAACC TCGGACAAAC
201     CGAAATCAAC CCGCAATTGC AGGCTTACGC CTGA

```

m263.pep (partial)

```

1 pep      (partial)
1  .. CGACGACGGG AATTTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
51  CCAAGCCGTA ATGGCGAAAA AAGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TCGGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151 GGC GT. AsyC TgGCAACCT GTGCAACTAC GTTCAACAAC TCGGACAAC
201 CGAAATCAAC CCGCAATTGC AGGCTTACGC CTGA

```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m263/g263

```

                                10      20      30
m263.pep                      AAGFDDAKLGALAAFTQAVMAKKGAVSDE
                                |||: ||||| ||||| ||||| ||||| |||:
g263      QCSFCVAGHTKLATLKKLLSEQSLNAARALAAAGKSDDAKLGALAAFTQAVMAKKGAVSDD
                                80      90      100     110     120     130

                                40      50      60      70
m263.pep      ELKAFFDAGYNQQQAVEVVMGVXLATLCNYVNNLGQTEINPELQAYAX
                ||: ||: ||: ||||| ||||| ||||| ||||| ||||| |||||
g263      ELNAFLEAGYNRQQAVEVVMGVXALATLCNYANNLAQTEINPKLQAYAX
                140     150     160     170     180

```

a263.seq

seq					
1	ATGGCAGCTT	TAACCGTACA	CACCCCTCGAA	ACCGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCC	CCCGAAGCCT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGCTCA	ACGCCGCCAA	CAGCCTGACC	CGCGCGGAAG	TGCAAGTAA
201	CCAGATTATT	GCCGCCCGCA	CCAACCAATG	CGGCTTCTGC	TGGGCAAGGC
251	ACACCAAACT	CGCAACCCCTG	AAAAAACTCC	TTTCCGAACA	ATCCGTCAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GTCGCGCGCC	TTTACCCAAG	CCGTAATGGC	AAAAAAAGGC	GCGGTATCCG
401	ACGAGGAATC	CAAAGCATTT	TTTGATGCGG	GCTACAACCA	CGACGAGGCA
451	GTCAGAGTGT	TGATGGCGCT	AGCCTTGGCA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCCGA	ATTGCAGGCT	TACGCTGA

a263.pep

```

1 MARLTVHTE TAPEAAKARV EAVLQNNQFI PNLIGVLSNA PEALAFYQEV
51 GKLANAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KKLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQA_
151 VEVVMGVALA TLCNYVNNLG QTEINPELQA YA*

```

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m263/a263 97.4% identity in 77 aa overlap

					10	20	30
m263.pep					AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAAARALAAAGEFDDAKLGALAAFTQAVMAKKGAVSDE						
	80	90	100	110	120	130	
		40	50	60	70		
m263.pep		ELKAFFDAGYNQQQAVEVVMGXLLATLCNYVNNLGQTEINPELQAYAX					
a263		ELKAFFDAGYNQQQAVEVVMGXLLATLCNYVNNLGQTEINPELQAYAX					
		140	150	160	170	180	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

```

1   ttgactttaa cccgaaaaac ccttttcctc ctcaccgccg cgttcggcac
51  acaactccctt cagacggcat ccgcccgcgc agtgggtcaag ccggaaaaaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgccgaatt cacgcaaacc
151 ggcacgcctt cgtggtacgg cggcagggtt caccggcgca aaacttcggg
201 cggagaccgc tacgatatga acgcctttac cgccgcccac aaaaccctgc
251 ccatccccag ccatgtgcgc gtaaccaaca caaaaaacgg caaaagcgtc
301 atcgtccgcg tcaacgaccg cggccccttc caccgcaacc gcatcatcga
351 cgtatccaaa gccgcgcgcg aaaaattggg ctttgtcagc caagggacgg
401 cacacgtcaa aatcgaacaa atcgtcccgg gccaatccgc accggttgcc
451 gaaaaaaaag acatctttat cgacttgaaa tctttcggtc cggaacacga
501 agcacaagcc tatctgaacc aagccgcccc aaatttcgcc gcttcgtcat
551 caagcccgaa cctctcgggt gaaaaacgcc gttacgaata cgttgtcaaa
601 atgggcccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggc
651 acgcggtatg gttcgggcgg tactgacctc cggttga

```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK PEKLHASANR SYKVAEFTQT
51  GNASWYGGRF HGRKTSGGDR YDMNAFTA AH KTLPIPSHVR VTNTKNGKSV
101 IVRVNDRGPF HGNRIIDVSK AAAQKLGFSV QGTAHVKIEQ IVPQGSAPVA
151 ENKDIFIDLK SFGTEHEAQA YLNQAAQNFA ASSSSPNLSV EKRRYEYVVK
201 MGPFAEQERA AEAEQAQARG MVRVLTSG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACCGCCG CATTCCGGCAG
51  ACACTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAG ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAATTT GGGCTTTGTC AACCAAGGGA CGGCACACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCAGTT GCCGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAACTTC GCCGTTTCGT CATCGGGTAC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 GCAGGAACGC GCCCGCGAAG CCGAAGCTCA GCGCGCGCGT ATGTTCCGGG
701 CGGTATTGAC CGCCGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGR FHGRKTSGBE RYDMNAFTA HKTLPISYV
101 RVNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAQKLGFSV NQGTAVKIE
151 QIVPQGSAPV AENKDIFIDL KSFGTEHEAQ AYLNQAAQNFA AVSSSGTNLS
201 VEKRRYEYVV KMGPFQSQR AEAEQAQARG MVRVLTAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHFGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHFGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAEQA QARGMVRVLTAGX					
g264	AYLNQAAQNFAASSSSPNLSVEKRRYEYVVKMGPFASQERAAEAEQA QARGMVRVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCAGAAAAC	CCTTTTCCTC	CTCACCGCCG	CATTTCGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAC
101	TGCACGCCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAC	AAGTCGCCGA	ATTCACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGGCGGCAGG	TTTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	CGCTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAAATCGTCC	CGGGCCAATC	CGCACCGGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTSGGE	RYDMNAFTA	AHKLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAQKLG FV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNP NLS
201	VEKRRYEYV	KMGPFASQER	AAEAEQA QARG	MVRVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m264.pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264.pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264.pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVRVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```
m265.seq
1  ATGTCGGTGA TTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGCGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGCGGAA
151 ATGCTCAGCA GTGCGGTGTC GGCGGAGGTC AAGAGAAGGT GTTGTATGTT
201 CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTCGGCTTC GGCGGCGCGT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```
m265.pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265.pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFI XFVNRGLENVDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
g265	TYSX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

```
a265.seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGGCGGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... .GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTCC TGGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

```
a265.pep
1  MSVILPPTRA NAAFAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKGAGHP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*
```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANA	AAFAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	LSSAVAAEV
a265	MSVILPPTRANA	AAFAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	PISAVAAAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIXFA	VNRGLENDIN	KVSNRQPAV	NTARTIPRAX	ASASAARSCE	VNGPILTT
a265	KRRRLKFI---	FAPAKYLXX	CLKDVKGAG	HPAVNTARTI	PRAXASASA	ARSCEANGPILTT
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

```
g266.seq
1  agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccacatcg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tggtcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgacg gagctggcgg caggtttcgc gctgaccgcc
201 tctcttgccg acatcctcga atcccgtagc ggagcggtac acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttgccttcc
301 cgtgtttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa
```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

```
g266.pep
1  MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT RTFGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGWEFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1  ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CCGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCTGTAC
301 CTGATTTTGG CGTTTCCATG TTTTGTGTGG CGGTATTTT GGCACACGCG
351 CAACAGGGAA TAG
```

611

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng)

from *N. gonorrhoeae*:

m266/g266

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
g266	MQFRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH					
	10	20	30	40	50	
	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX					
	:					
g266	LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX					
	60	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTG CTGCTGCCT
101  TGATTTTTC CAACGCCCC TTCCTACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TCGCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC GGTTCCTCTG TTTCTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLEGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
a266	MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLGIVPLKRKHFGHH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	:					
a266	LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	70	80	90	100	110	120
m266.pep	X					
a266	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq

This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

1 MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGOVDVV TLGAAGAVFA  
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLPGKI  
101 NCVFAGKKVF ERYAHAFDQF AKQKGFY\*

```

1      GTGCAAGTCG CCTTTTTTCT CGCCGTGGTA TTCAAAAATA TGGGTTTCCA
51     CAATCGCATC AGTCGGGCAT GCCTCTTCGC AGAAACCGCA GAAGATGCAC
101    TTGGTCAGGT CGATGTCGTA ACGCTTGGTG CGGCGCGTAC CGTCTTCACG
151    TTCTTCCGAT TCGATGTAA TCGCCATTGC CGGACACACT GCCTCACACA
201    ACTTACACGC GATACACCGC TCTTCGCCGT TCGGATACCC CcGCTCGCGG
251    TGCAGACCCG GGAACGCAC GGAATTGCGG GTTTTCTCTT CGGGGAAATA
301    AATTGTGTCT TTGCGGGCGA AAAAGTTTTT GAGCGTTACG CCCATACCTT
351    TTACCAATTC GCCAAGCAGA AAGGTTTTTA CTA

```

1 VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGQVDVV TLGAARTVFT  
51 FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI  
101 NCVFAGEKVF ERYAHTFYQF AKQKGFY\*

from *N. gonorrhoeae*:

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFKNMGFHNRI	SRACLF	AE	TALGQVDVVTLGAARTV	FTFFRFDVNRHC	
		:				:	
g267		MQVAFFLAVVFKNMGFHNRI	GRAGLF	AE	TALGQVDVVTLGAAGAVFAFFRFDVDRHC		
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTP	PLFAVRI	PPLRVQTAETHGLRRFL	FG	GEINCVFAGEKVFERYAHTFYQF	
g267		RTHRLAQFT	RDAAFLSVRK	TALRVQTAETHGLRRFL	FGKINCVFAGKVFERYAHAFDQF		
		70	80	90	100	110	120
m267.pep		AKQKGFYX					
g267		AKQKGFYX					

seq					
1	GTGCAAGTCG	CCTTTTTTCT	CGCGTGGA	TTCAAAATA	TGGGTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCTTTTCCG	AGAAACGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTTGGT	CGGCGCGTGC	CGTCTTCGG
151	TTCTTCAGAT	TCGATGTTGA	TCGCCATTGC	GGGGCAAACG	GCTTCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	GC GTTGC GCG
251	TGCAGACCGC	GGAAACGGCA	GGATTTCGGC	GTTTCTCTT	CGGGAAAAATA
301	AATCGTGTCT	TTGCGGGCAA	AAAGTTTTTT	GACGCTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFF	FRFDVNRHC		
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFF	FRFDVDRHC		
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTP	PLFAVRIPLLRVQTAETH	GLRRFLFGEIN	CVFAGEKVFERY	AHTFYQF	
a267	GANGFTQFTRDAA	FLAVWITALRVQTAETH	GLRRFLFGKIN	RVFAGKKVFER	AHTFYQF	
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tgggtcaaact ggtccgagac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggctgaaac
251 gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccagacg
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaaagcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgagggg
651 ggcagaagaa gcggcgccgc agggagcatt gggtcgggag caggaaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccaaacaatg
851 cgaaagccga aggtgaaacg ccaaaccgca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcagcgttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLIGINPFSG KEISCGSEET KEILVKLVDRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAAL KLDVPPDDVD YAVAAQSIG NSHKKTPDFF EPYYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAREAE EAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKIQASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```



614

```

51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGCGC
151 AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAACn TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGCAGGGAA GCGGACAmGA
401 AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

m268.pep (partial)

```

1  ..MALIKEPLDK VKQRNEELEA AEEAAAEAL GREQEAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEA-----
                                |||:|||:|||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAEALGREQEAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLPQSQTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLPQSQTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

a268.seq

```

1  ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGCGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

a268.pep

```

1  MALIKEPLDK AKQRNEELEA AEEAAAEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAEEAAAEALGREQEAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAEEAAAEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
m268.pep	70	80	90	100	110	120
	PQTVQNKLOPSQKTWKSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
a268	PQTVQNKLOPSQKTWKSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	70	80	90	100	110	120
m268.pep	130	140				
	KALIDEMXREADXKELSKRLX					
a268	KALIDEMXREADXKELSKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCCCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHCSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAAARVSE EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

	10	20	30
m268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKVKQRNE		
	:	:	:
g268	KEGAYVYKTISSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE		
	150	160	170
	40	50	60
m268-1.pep	ELEAAE-----EAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN		
	:	:	:
g268	KLEAAEATAQEAREAEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN		
	210	220	230
	90	100	110
m268-1.pep	KLQASQKTWKSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE		
	:	:	:
g268	KLQASQKTWKSGMDKICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRKKALIDE		
	270	280	290
	150	159	
m268-1.pep	MAREADKKELSKRLX		
	:	:	:
g268	MVREEDKKELPKRLX		
	330		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCCCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

616

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC  
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep  
 1 VQSRDGLHK FKHCSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR  
 51 EQEVDVRSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI  
 101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD  
 151 KKELPKRL\*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKAKQRNEELEAAEAAAAQALGREQEVDRVSEW					
m268-1	VQSRDGLHKFKHCSAAMALIKEPLDKVQRNEELEAAEAAAAQALGREQEAARVSEW					
	10	20	30	40	50	60
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEKTPNGIKFSEL					
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEKTPNGIKFSEL					
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKALLDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq  
 1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc  
 51 cagcccttgg atttggcgcg tggtgtgggt gtggtcgcg tcggcttttt  
 101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttgccg  
 151 gtttcgccgt gggactttat ccggaacacg gcttcgccc aagtggtcggc  
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc  
 251 cggcgttgcc cattttgctg tccaatcgcg gggtaaaaa accggtgtcg  
 301 ttttaagtcgc cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc  
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep  
 1 MVWRVNCAAT AALIFSSSPW IWAUVVWWSR SAFSCKPCAS LDASSAPALA  
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS  
 101 FKSPSVQVDT SALLCLSLRS S\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq  
 1 ATGGTTTGGC GTGTGAATTG CGCGCAACG GCGGTGCTGA TTTTTCGTC  
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGTCTCGG TCGGCTTTGT  
 101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCCTGC GTTGATGGTT  
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC  
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC  
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT  
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT  
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep  
 1 MVWRVNCAAT AVLIFSSSPW IWAUVVWWSR SALSCKPCAT CPRPAPALMV  
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF  
 101 KFSSVQVDT SALLCLSLRS \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng)

from *N. gonorrhoeae*:

```

m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269      MVWRVNCAATAALIFSSSPWIWAVVWVWSRFAFCKPCASLDASSAPALAVSPWDFIRNT  60

m269.pep  ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTSAALLCLSLRS  119
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269      ASPKVSAAALMHSEKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDTSAALLCLSLRS  120

m269.pep  SX  121
          ||
g269      SX  122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CCGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCCTGT CCAGCGCGCC GCGGTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGCGCG TTTTCGTTCG
251 CGCCTGTTCG CATTGTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTGTTCG
301 TTTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1096; ORF 269.a&gt;:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAAAL HSEKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269.pep  10 20 30 40 50 59
          MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
a269      10 20 30 40 50 60
          MVWRVNCAATAVLIFSSSPWIWAAVWVWARSALSWRFCASVPASSAPALTVSPWDFIQNT

m269.pep  60 70 80 90 100 110 119
          ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTSAALLCLSLRS
a269      60 70 80 90 100 110 120
          ASPKVSAAALMHSEKTRALGRFSSPPVAILLSRGVKKPLSFKFSSVQVDTSAALLCLSLWS

m269.pep  120
          SX
          ||
a269      120
          SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcaactgctgc tgactgcctt
51 tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgcgcg cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccc cggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg gggttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcac cgctgcccgc tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1098; ORF 270.ng&gt;:

g270.pep  
 1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ  
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq  
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG Ca.CAGCCGC  
 101 AAGCTGTGGC GGCACAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCGGTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA  
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep  
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ  
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng)

from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAFKLVLLQWWQAQQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq  
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG CAGCAGCCGC  
 101 AAGCTGTGGC GGCACAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA  
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep  
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALLL	IAFAAVK	LVLLQW	QAXQPQ	AVAAQC
a270	MNKNRKL	LLAALLL	IAFAAVK	LVLLQW	QAXQPQ	AVAAQC
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDI	YIEHAP	AGTEQV	SISFSM	KNMDMG	FNRYMF
a270	TKKPFDI	YIEHAP	AGTEQV	SISFSM	KNMDMG	FNRYMF
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADIT	IGSRTF	QTAFTA	EX		
a270	DFTADIT	IGSRTF	QTAFTA	EX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1 atgttcagtt cgcggtatggc gaggatttgg gcgacggggg taacgttgtg
51 tatggtcagt ccgtgtccgg cgctgacgac caagcccaaa tcgccggcga
101 aatgcgcgcc gttttggatg cgctcgaaact gcctgatttg ttcggcgtgg
151 ctttgtgcgt cggcatatgc gccggtgtgc agctcgacaa cgggcgcgcc
201 gacatcacgg gcggcttggg tttgcctgtc gtcggcatcg ataaacaagg
251 acacgcgtat gcccgcgctc gtcaggattt tggcgaattc ggcgattttt
301 tcctgttgcg ccaatacgtc caaaccgcct tcggtcgtga tttcctgccc
351 tttttcaggc acgatgcaca cgtcttccgg catcacttta agcgcgtttt
401 cgagcatttc ttccgtcaac gccatttcaa gggtcaggcg cgtgcggatg
451 gcgtttttga cggcaaatat atccgcgtct ttgatgtggc ggcggtcttc
501 gcgcaggtgc atggtaatca ggtctgcacc gtgcgtttcg gcaaccagtg
551 ccgcctccac ggggctggga taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

m271.pep

```

1 MFSSRMARIW ATGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51 LCASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILANSAIF
101 SCCANTSKPP SVVISCRFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1 AwGTTcagTT CGCGGATGGC GAGGATTtGG GCGATGGGGG TAACGTTGTG
51 TATGGTcAGT CCGTGTCCGG CGTTGACGAC CAAGCCCAAA TCGCCGGCGA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTtG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTGGG TTTGCCTGTC GTCGGCATCG ATAAACAAAG
251 ACACGCGTAT GCCTGCGTCG GTCAGGATTt TGGTGAACCC GGCGATTtTT
301 TCCTGTTGCG CCAATACGTC CAAACCGCCT TCGGTGCTGA TTTCTGACG
351 TTTTTCAGGC ACGATGCACA CGTCTCCGG CATCACTtTC AAAGCGTtTT
401 CCAACATTTC TTCCGTCAAC GCCATTtCAA GGTTcAGGCG CGTGCGGATG
451 GCGTtTTTGA CGGCAACAC GTCCGCGTCT TTGATGTGGC GGCgGTCTTC
501 GCGCAGGTGC ATGgTAATCA AATCCGcACC GTGCGTtTCG GCAACcAGTG
551 CCGCCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1 XFSSRMARIW AMGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51 LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNPAIF
101 SCCANTSKPP SVVISXRFSG TMHTSSGITF KAFTNISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIKSAPCVS ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTS KPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAAPCVS					
g271	TMHTSSGITLSAFSSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTCA GTT CGCGGATGGC GAGGATTGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT CCGTGTCCGG CGTTGACGAC CAAGCCCAA TCGCTGGCAA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTG TTCGCGGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTGGG TTTGCCTGTC GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT GCCCGCGTCG GTCAGGATT TGGTGAATTC GGCAATTTTG
301 TCTTGTGCG CCAATACGTC CAAGCCGCCT TCGTCTGTA TTTCCTGACG
351 TTTTCCGGC ACGATGCACA CGTCTTCCGG CATCACTTA AGCGCGTTTT
401 CGAGCATTTT TTCCGTCAAC GCCATTCAA GGTTCAGGCG CGTGCGGATG
451 GCGTTTTTGA CAGCAAACAC GTCCGCGTCT TTGATGTGGC GCGGCTCTTC
501 GCGCAGGTGC ATGGTAATCA GGTCCGCACC GTGCGTTTCG GCAACCAAGT
551 CCGCTCCAC GGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTS KPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTS KPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcgatgg ctgcgccata tgaacaaaaa
51  caaaggttcc gacctgtttg tgacgacca tttcccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtgca atttcgccat cagcctgcgg gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgcgc tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctccgggcaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaa gattccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggttg aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctccgaccga tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgcctcgctc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttcgct
1051 ttggcggtac agttgcgcag ccgcagggca caaagtccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTTFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAPFIMS AKQAEFFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQ EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLGMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMOF FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAAGT GTTCGCATGG CTGCGCCATA TGAWCCAAAA
51  CAAAGGTTCC GACCTGTTCC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCCTGAC GGC GGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAACG CGGGCTGTT ATTTTGTTCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG

```



```

551 TGGATACGGA AAACCTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTCCCGGAG
751 GAGCGGCGCG AACAAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTGCGAGTT GATTCACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTCCCTGCA AGAAGCATTG AAAAAATGCG ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCGGATTT
1101 GGNACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMxQNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVAM IQRGATALVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGQMT FDQHLQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

	10	20	30	40	50	60
m272.pep	MTAKEELFAWLRHMxQNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	:					
g272	MTAKEELFAWLRHMKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m272.pep	AKQAEFSSTNECNFAISLPDTSRFRVAM IQRGATALVFRTITSKIPKFESLNLPVVK					
	:					
g272	AKQAEFSSTNECNFAISLPDTSRFRVAM IQRGATALVFRAITSKIPKFESLNLPALK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m272.pep	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLCMATLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLCMATLHANSTNQA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
g272	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGQMTFDQHLQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGQMTFDQHLQLYEKGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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m272.pep                    370  
                               QSXSPDLXLLX  
                               || :||| |||  
 g272                        QSSDPDLELLX  
                               370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

a272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAACG CGGGCTGGTT ATTTTGTGTC
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAACGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCCGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATT
1101 GGAACGCTC TGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

a272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTGSGK STSLASLIDY
151 RNENSGHII TIEDPIEFVH EHKNCIITQR EVGVDENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMOF FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *
  
```

m272/a272 97.6% identity in 370 aa overlap

	10	20	30	40	50	60
m272.pep	MTAKEELFAWLRHMNKNKGS DLFVTHFPFAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
a272	MTAKEELFAWLRHMNKNKGS DLFVTHFPFAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRTITSKIPKFESLNLPVVK					
a272	AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRAITSKIPKFESLNLPVVK					
	70	80	90	100	110	120
m272.pep	DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSGHII TIEDPIEFVHEHKNCIITQR					
a272	DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSGHII TIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFFPEERREQLTDL SLN LQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLTDL SLN LQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272.pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```

g273.seq
1  atgagtccttc aggcgggtatt tatataccccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcaccc ttttctgcc gtttctgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcggcgca gccgcgccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcggcgcc gtgcgcgtga aatcaaggcg
351 gtttgagaag tgttccnacc gcgcccgcgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccct cttttgttt ttcaagcagt
501 tttttcttac gcgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```

g273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGKAHKQ QSGKHTDRR QDIGVFEAGT
51  PPTVFLPLV AFEIKDDAGK QRSRRARWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRREFK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```

m273.seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCTCCG TTTCTCTGCC GCTTCTGTG GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTTCATT
251 GTTGTTCTCTT AATGCTTAAA AACC CGCCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAATTG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTGTG
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGKTWTC AAGCAGTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```

m273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGKAHKQ QSGKHADRC QDIGVFKAGT
51  PPFVFLPLV AFEIKDDAGK QRSRRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/q273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSR	TAQYNENQENG	GKAHKQ	QSGKHADRC	QDIGVF	KAGTFPFVFLPLL
g273	MSLQAVFIYPPSR	TAQYNENQENG	GKAHKQ	QSGKHADRR	QDIGVF	EAGTFPFVFLPFL
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQ	RSRARHXC	CVHCCSLML	KNPPVRAT	VLRRQIAK	FVCGRVLKSG
g273	AFEIKDDAGKQ	RSRARHWH	CVHCCSLT	VKNPPGRAT	VLRRREIA	KFVCGRVLKSR
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRA-ALCAG	VICRSPAK	SPRTRFAE	FPCHPLVS	YGYYLPFV	XQAVESYAX
g273	CFXRARPMCR	NIICRSPAK	SPRTRFAE	FPCHPLVS	YGYYLPFV	XQAVESYAX
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

seq					
1	ATGAGTCTTC	AGGCGGTATT	TGTATACCCC	CCAAGCCGTA	C CGCACAAATA
51	CAACGAAAAT	CAGGAAAACG	GCGGTAAAGC	TCATAAACAG	GGACAAAGCG
101	GCAAACACGC	CGACCGCCGT	CAGGATATAG	GCGTATTCCA	GACCGGAACT
151	CCATTACCG	TTTTCTGCC	GCTTTTGTC	GCTTTTGAAA	TAAAGGATGA
201	TGCCGGCAAG	CAGCGCGGCA	GCCGCGCCCC	ACATTAGCAT	AATGTTTATT
251	GTTGTTCTT	AACGTTTAAA	AACCCGCCCG	TCCGTGCAAC	CGTTTTTAAAG
301	AGGCGGTAAA	TCACAAAGTT	TGTTGGCGGA	CGTGCTCTAT	TACAATCAGG
351	GCGGTTTAA	GGGCATGATG	CAGTGCCCCG	TGTGCCGGAT	ATTATTGTGTC
401	GCTCACCTGC	AAATATTGCCA	AGAACC GCCT	TTGCGGGATT	TCCACATTGC
451	CCACTTGTTT	CATACGGCGT	TTGCCTGCTT	TTTGT TTTTC	AAGCAGTTTT
501	TTCTTACGCG	TAA			

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP  PSRTAQYNEN  QENGGKAHKQ  QSGSKHADRR  QDIGVFQTGT
51  PFTVELPLFV  AFEIKDDAGK  QRGSRARH*H  NVHCCSLTVK  NPPVRATVFK
101 RR*ITKFVGG  RALLQSGREF  GHDALPRVPD  IICRSPAKLP  RTRFAGFPHC
151 PLVSYGVCLL  FVFQAVFSYA  *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKHQGQSGKHADRCQDIGVFKAGTFFPVPFLPLL					
a273	MSLQAVFIYPPSRTAQYNENQENGGAHKHQGQSGKHADRRQDIGVFQGTGTFTFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRRARHXHCVHCCSLMLKNPFPVRATVL-RRQIAKFVCGRVPLKSGRFL					
a273	AFEIKDDAGKQGRSRRARHXHNVHCCSLTVKNPFPVRATVFKRRXITKFGVGRALLQSGRFLK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRRAALCAGVICRSPAKSPRTFAEFPHCLPVSYGVLFPVXQAVESYAX					
a273	GHDALPRV-PDIICRSPAKLPRTFRAGFPHCLPVSYGVCLLFVFQAVESYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGGGc ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCCT
351 TCCGCCGCC AACCCTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AGGCAATGC GGTGATTG
451 ACCCCGATGG ACAACTTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFBG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQGNVAVL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAACATAT CGACATCCAG CTTATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGGGc GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFBG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTSLPT NHWYVRVEDA AGVWRVENKW ITSQGNVAVL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
m274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFBG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLPPA					
m274	DMNAAKVFBG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDA AGVWRVENKW ITSQGNVAVL TPMDKLFN NAGSKX					
m274	NHWYVRVEDA AGVWRVENKW ITSQGNVAVL TPMDKLFN NTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GCGCGCTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTGG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m274.pep	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQGNVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQGNVDL TPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tggcgacga tgaatgccgt gcggttttcc atcaggcgtt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgctcaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgctc ttcaaatgg cgcgggcat
201 ggcgacgctg tgcgctgtc cgcgggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgagc ggggatgcgt cgatcaggct ttgcaggttg
301 gcggtcttga gggcgacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggacg ttttcaaaca ggggtgctgc aaacaggaa acgtcttggg
401 agacgagggc gaattgggcg cgcaggcagt cgagttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaagggtg acgacggtg atttccgct gccggaacgt cgcaccaggg
551 cgacgcgttc gccttgctg atgtcgaggt tgaagtgtc gagggcttgg
601 atgctgctg aacggtattc gacatcgac ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcgcgcgca gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcgcgca ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatggg gcgtacatt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

m276.seq

8	1	ATGATTTTGC	CGTCGTCCAT	CACGATGATG	CGGTCGGCCC	CTTCGATGGT
	51	GGTCAGGCCG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTCC	ATCAGGCGTT
101		CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCTAA	TGCGCTGGTG
151		GCTTCGTCCA	ATAAATAAT	CGGCCGGTCT	TTCAAATGG	CGCCGGCAAT
201		GGCGACCGCT	TGCCGTGTC	CGCGCGATAA	GTTGCTCCGG	TTCGATCCGA
251		TGGGCTGGTG	CAGTCCGAGC	GGGGAGCTGT	CAATCAGGCT	TTGAGGTTG
301		GCGGTTTGGA	GGGCGAACAG	GACTTCGGCT	TCGCCCCGCT	CGGGACGGCT
351		GTATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTTGGG
401		AGACGAGGGC	GAATTGGGCG	CGCAGGCAGT	CGAGTTTGAT	GTCGCGCATG
451		TCGATACCGT	CTATGCAGAT	GTTTCCGGCA	GACGGTTCGA	CAAGCGGGG
501		CAGCAGGTG	ACGACGGTGG	ATTTCCGCGT	GCCGGAACGT	CCGACCAGGG
551		CGACGCGTTC	GCCTTGCTCTG	ATGTCGAGGT	TGAAGTTGTC	GAGGGCTTTG
601		ATGCCGTCTG	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATGCGCCC
651		TCGACACGCG	TGCGGTGCGA	TGCTGCCCTT	GTCTGTTCG	GGCGGGGTGT
701		CGAGAAATGC	ACATACACCG	TCGGCGGGCA	GGAACATCGT	CTGCATAGGG
751		ATGCTGATGT	TGGCAAGGCT	TTTGATGGGG	CGGTACATT	CGGACATCGC
801		GACGATGAAT	GCCATAAATT	CGCCGATGGT	GGTGTAG	

m276.ppt

```

1  MILPSSITMM RSAPSMVVRW WATMMPVVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGLRYLT FSNRVSSNRN TSWETRANWA RRQSSLSMAS
151 SIPSMQMLPA DGSTKRGSRLL TVDVLPLPER PTRATRSPL MRSLKLSRAL
201 MPSERYLST LRKLMPRTS CGASVPLSCS GGVSRNAPT SAARNVICIG
251 MMLRLALMST AYICISATMNN AINSMPVV*

```

Homology with a predicted ORF from *N.gonorrhoeae*

from *N. gonorrhoeae*:

m276/q276

	10	20	30	40	50	60
m276.pep	MILPSSITM	MRSAPSMV	VRRWATMM	PVRF	SIRRSSACW	TRRSDSLSNALVASSNNNIGAS
g276	MILPPSMTM	MRSADSTV	VRRWATMM	PVRF	SIRRSSACW	TRRSDSLSNALVASSNNNIGAS
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMAT	RCRCPPDK	LPLFPDPM	GWCS	PSPGELSIR	LCRLAVWRANRTSASPASGRLYRT
g276	FKMARAMAT	RCRCPPDK	LPLFPDPM	GWCS	PSPGDASIR	LCRLAAWRADRTSASPASGRLYRT
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNR	NTSWETRAN	WARRQSS	ILMSAMSIP	SMQMLPAD	GSTKGRSRLTTVDLPLPER
g276	FSNRVSSNR	NTSWETRAN	WARRQSS	ILMSAMSIP	SMQMLPAD	GSTKGRRLTTVDLPLPER
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCL	MSRLKLSR	ALMPSE	RYSTSLR	KLMRPSTR	CGASVPLSCSGGVSRNAHTP
g276	PTRATRSPCL	MSRLKLSR	ALMPSE	RYSTSLR	KLMRPSTR	CGASVPLSCSGGVSRNAHTP
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```

a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTGCTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGCG AAATTGGGCG CGCAGGCAGT CGAGTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGCGA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCCGCC
651 TTCGACACGC TCGGGTGC GA GCGTGCCCTT GTCCTGTTG GCGGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATTT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
  
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```

a276.pep
1  MILPSSITMM RSAPSMVRR WATMMPVRF IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RQSSILMSAM
151 SIPSMQMLPA DGSTKRGSR TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
  
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVRRWATMMPVRF IRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVRRWATMMPVRF IRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLLTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLLTVDLPLPER					
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLLTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLLTVDLPLPER					
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					



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250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
  1 ..atgggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttggcc
 51 aaacgaggtc atagacgttt tccacgcctt gcaggtacat cgccaagcgt
101 tcgatgccgt aggtaatttc gccgagtagc ggcgtgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccaccac gcaccgaggg tgggggtttc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgcag
301 ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgagggcga
351 cttggaattg gtaatagtgt tgcaggcggg tgggggttgc gccgtagcgg
401 ccgtctttgg ggcggcggct ggggttgagc taggcggcaa accaaggctc
451 ggggcccagc gcgcgcagcc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttgg atgacggtgc agcctttgtc tgcccagaag
551 gtttgcagtt tgaagatgat ttgttgaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
  1 ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
 51 DLLEIGKLG YFHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVLDI GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPRL
151 GAERAQAGG MGCAGTDFHV EGLDDGAAFV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
  1 ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
 51 TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAC TGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTTC AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT AACTGGGTT ACTTCCATGC
351 CGTTGAGCCA GACTTCCCAG CCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGCACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCCGCG AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTGCA GTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GCCTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
  1 MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG IAVFEVVGGLL
 51 DFVLVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG YFHAVEP DFPAQTPRAE GGVFPVVF DADVVDFGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAV FGAAGLDVGG
201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30  
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH

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```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVGDGVAVERFCPNEVVDVFTLQVH
           30      40      50      60      70      80
g277.pep  RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAFEPDFPAQTPTREGGVFPVVFADKADV
           40      50      60      70      80      90
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEPDFPAQTPRAEGGVFPVVFADKADV
           90     100     110     120     130     140
g277.pep  DFGIDAQFAQGVEIEVLIDIGGGFEGDLELVIVLQAVGVVAVAVFGAAAGLDVGGKPRL
           100     110     120     130     140     150
m277      DFGIDAQFAQRVEIEVLIDIGSGLEGDLELVIVLQAVGVVAVAVFGAAAGLDVGGKPRL
           150     160     170     180     190     200
g277.pep  GAERAQAGGGMGCAGTDFHVEGLDDGAAAFVCPEGLQFEDDLLEGKHGLL
           160     170     180     190     200
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51 TTTCTTCGGC AAGCAGGCGT TTGGCTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGATTGTTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCAGTCGT CTTCGACAAA GCGGATGTCG TGCACTTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGATATTG GCGGGAGCGG
501 GCTTGAGGCG GACTTGGAAT TGGAATAGT GTTGAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTCAG TTTGAAGATG ATTGTGTTGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDA ADVVHFGVDA
151 QFAQGVEIEV LDIGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

m277.pep  10      20      30      40      50      60
MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLD FVLVVHVAV
|||||
a277      10      20      30      40      50      60
MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLD FVLVVHVAV
|||||

m277.pep  70      80      90      100     110     120
GDGVAVERFC PNEVVDVFTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEP
:  ::|||
a277      70      80      90      100     110     120
SYCITVQRFC PNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
|||||

          130     140     150     160     170     180

```

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```

m277.pep    DFPAQTPRAEGGVFPVVFADKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVILQA
            |||||
a277        DFPAQTPRAEGGVFPVVFADKADVHFGVDAQFAQGVIEIEVLDIGGSGLEGDLVLVILQA
            130      140      150      160      170      180

            190      200      210      220      230      240
m277.pep    VGVVAVAAVFGAAAGLDVGGKPRLGAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCP ECLQ
            |||||
a277        VGVVAVATVFGAAAGLDVGGKPRLGAECAQTGGGMGCAGTDFHVEGLDDGAAAFVCP ECLQ
            190      200      210      220      230      240

            250
m277.pep    FEDDLLEGKHGLX
            |||||
a277        FEDDLLEGKHGLX
            250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq    (partial)
1    ttgcgtgcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaat
51   tgtattaatc ggacctttgc cgtcgatagg cggacccaat gcatcgacga
101  cgcgtccgac caattcgcgt cgcaccggca cttctaaat acggccggta
151  caggtaaccg tgcgccttc ttaatatgt tcgtactcgc ccaacactac
201  ggcaccgacg gagtgcgcgt ccaggttcat cgccaagcct aaagtgttac
251  ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301  cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351  ggcattttaca gacagatttt cgatcttggc ttaatcaga tcgctaattt
401  cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451  caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501  cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep    (partial)
1    LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51   QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101  RTIPSVTEIT VPRVLTSAFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151  QSTQFALYRQ IQNLITHFNF....

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1    TTGCGCGCAA TCACGCCCGG TGCATTTTTT TCGATAGGGG CGGTCAAAGT
51   TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101  CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151  CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201  GCGCGCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251  CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301  CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351  GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401  CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451  CAAGGCACTC AATTGTCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501  CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551  TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601  CTGTTTGTGCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651  GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1    LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51   QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101  RTIPSVTEIT VPQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151  QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLHLAD
201  LFVQQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

633

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng)  
from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC				
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYSNPTTAPTESRSR	FIAPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPRVLTSAFT			
m278	SYSNPTTAPTESRSR	FIAPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPRVLTSAFT			
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGLS	CMKTLIRHSRVQSTQFALYRQ	IONLITHFNF			
m278	DRFSILALIKSLISAGLS	CMKTLIRHSRVQGTQFALYRQ	IONLITHFNFYANQLRFDF			
	130	140	150	160	170	180
	190	200	210			
m278	DRDFQLAVETLIQHLHQL	ADLFVQGRI	GTVDGRFDMVE*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

```

1  TTGCGCGCAA TCACGCCCGG TGCATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GCGCGCCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSNPTTAPT ESRSRFIAP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSM KTLIRHSRV
151 QGTQFALYRQ IONLITHFNF YANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVQGRIQTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC				
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYSNPTTAPTESRSR	FIAPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPRVRTSAFT			
a278	SCSNPTTAPTESRSR	FIAPKVLPGNSSISPCIASDKP	WMRTIPSVTEITVPRVRTSAFT			
	70	80	90	100	110	120

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	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLHLQADLFVQGRIGTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLRLQADLFVQGRIGTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 cgggcagcgg cagggcgctg ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcgccggc gttgcctgca atcacgactt gtccggcgca
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcactt tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTSS SKPKMAAIAP
101 TPCGTADCIS SARRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTGCG GCGGCGGTTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACC GGCTTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTGCA ATCAGGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATGCGCCCC
301 ACGCCTTGCG GTACGGCGGA CTGATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTGCGCGAG GCTGTGTCCG GCAACGCGG CAGGCGTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITTCPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRTSLTA SAKFNAPAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:     : :     :     :     :     :     :     :     :     :					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

m279.pép ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSTLTA  
|| ||||||| | ||| : ||||| : |||||||  
g279 ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRSTLTA  
70 80 90 100 110 120

130 140 150  
m279.pép SAKFNAPAATS AVYSPRLCPATAAGVLP PASKX  
||| || ||||||| ||||||| : |||  
g279 SAKSNASAATS AVYSPRLCPATAAGVLP PTSPKX  
130 140 150

```
a279.seq
  1  ATGACNCGA TTTGCGGCTG CTTGATTTC ACGGTTTNA GGGCTTCGGC
51  GAGTTTGTCT GCGGCGGGTT TCATGAGGCT GCAATGGGAA GGTACNGACA
101 CNGGCGACGG CAGGGCGCGT TTGGCGCCGG CTCCTTTGGC GCGCAAGCAT
151 GCGCGCTCGA CGGCGCGCGC ATTGCGCTGA ATCACGACTT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTC CTGTTTCATC TCCAGCCGA GAATCGCCGC CATTCGCCCC
301 ACGCCTTGCG GTACGCGCGA CTGCATCAGT TCGGCGCGCA NGCGCACAGG
351 TTTGACC CGC TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGCGCG CAGCGCTTTT GCGCGCCGCT
451 TCCGAATAG
```

```
a279.pep
1  MTXICGCLIS TVXRASASLS AAGFMRLWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAT SAVYSEXPCLP ATAAGVLPFA
151 SE*
```

```

m279.pep      ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA
a279           :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
               10      20      30      40      50      60

m279.pep      MTXICGCLISTVXKRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA
a279           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
               10      20      30      40      50      60

m279.pep      ITICPGELKLTASTTSLWAASQAQMALTCSSSKPRIAAIAPTCPGTADCISSARRRSTLTA
a279           || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
               70      80      90      100     110     120

m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPASKXX
a279           ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
               130     140     150

m279.pep      SAKSNAPAATSAVYSPXLCPPATAAGVLPASEX
a279           ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
               130     140     150

```

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaaccttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca cccttccgg ttgtaaccag tttagcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgctga aacctgata aaggccgac ccgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgacacagca cgcaaacgca gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtccctga cggggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtag cagcgaagcc gagccgtccg
701 ccaaacaaagt cgccgccatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtt accgcactcg
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EGGHHHDH HDHHDHDEGH HDHDEYDPH VWNDFVLMDS
151 YAQNVAETLI KADPEGKVYY QQRILNYQMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQGSSEA EPSAQVAAI IRQIKREGIK
251 AVFTENIKDT RMDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACTCAC CTTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTAGCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCACT GCAAACTCG TCCTGCTCAA CCGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GCGGAATATG
401 ACCCGCAGT CTGGAACGAC CCCGTCCTTA TGTCCGCTTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGTG CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCTTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EGGHHHDH HDHDEGHHDH GEYDPHVWND PVLMSAYAQN
151 VAKALIKADP EGKVVYQQL GNYQMLKKL HSDAQAAFNA VPAKRKVLV

```

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAIIIRQI KREGIKAVFT  
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN  
 301 AMKQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)

from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSFILGDAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTLIAALLATAATAAPLPVVTFSFILGDAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDH-					
	::					
g280	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNPVLM SAYAQNVAKALIKADPEGKVYYQQLGNYQMQ					
	::					
g280	HDHDHDHEGHHHDHGEYDPHVWNPVLM SDY AQNVAETLIKADPEGKVYYQQLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSEAEPSAKQVAAI					
	::					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSEAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AAC TGCCGCC	CCCCTGCCGG	TTGTAACCA	CTTCAGCATT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCATACAAAG	TTTGGTCGGA
151	GCCAAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGGCG	ACATTAAAAA
201	AATCCGCAGT	GCAAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCCT	TATGTCCGCC
451	TATGCCCAAA	ACGTGCCCGA	AGCCCTGATA	AAGGCCGACC	CCGAAGGCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCCGCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGC



638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG  
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA  
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep  
 1 MKHPKLTLLIA ALLTTAATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG  
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA  
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDFVLMSA  
 151 YAQNVAEALI KADPEGKVYY QQLGNYQMQ LKKLHSDAQA AFNAVPAAKR  
 201 KVLGTGHDAFS YMGKRYHIEF IAPQGVSSSEA EPSAKQVAAI IRQIKREGIK  
 251 AVFTENIKDT RMVDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNK  
 301 ALTNAMKQ\*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLLIAALLTASATAAPLPVVTSFSILGDVAQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHPKLTLLIAALLTTAATAAPLPVVTSFSILGDVAQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	TSGDIKKIRS AKLVLLINGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRS AKLVLLINGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
m280.pep	TSGDIKKIRS AKLVLLINGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRS AKLVLLINGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
m280.pep	HDH----EGHHHDHGEYDPHVWNDFVLMSAYAQNVAKALIKADPEGKVYYQQLGNYQMQ					
a280	HDHDHDHEGHHHDHGEYDPHVWNDFVLMSAYAQNVAEALIKADPEGKVYYQQLGNYQMQ					
	130	140	150	160	170	180
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
	190	200	210	220	230	240
m280.pep	IRQIKREGIK AVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIK AVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	240	250	260	270	280	290
m280.pep	IRQIKREGIK AVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIK AVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	250	260	270	280	290	300
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq  
 1 atgcactacg ccctcgcacg cgtcttctgc ctgtccctca gcgcgcgacc  
 51 cgtcggcgta ttcctcgtca tgcgccgat gagcctgata ggcgacgcat  
 101 tgagccacgc cgtcctgccc ggtgccgccc tcggctacat gtttgccggc  
 151 ttgagcctgc ccgctatggg tgtggcgggg tttgccgccc gtatgctgat  
 201 ggcgctgctt gccgactcgc tcagccgctt taccaccctg aaagaagatg  
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc  
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc  
 351 tgtgcttgcc gtcgatattc ccgactgca actcatcgcc gccgtctccg  
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa  
 451 agcatagacc cccttttctt caagtccgct aacggcaaa gcgggctttg

639

501 gcacgtcatt ttcctcatcc tcgtcggttat gaacctcgta tccggcttcc  
 551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt  
 601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgttgctcgt  
 651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca  
 701 tcgaaatccc ttccggcccc gccatcatcc tctgttcag cgtcctttat  
 751 cttttttccg tcatactcgg caaagaaggc ggcatcttgc ccaaatggtt  
 801 caaaaaccac cgccaccaca ccacctga

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

1 MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG  
 51 LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL  
 101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE  
 151 SIDPLFLKSV NGKGGWLWHVI FLVLVVMNLV SGFQALGILM SVGIMMLPAI  
 201 TARLWARNMG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AIILCCSVLY  
 251 LFSVILGKEG GILPKWFKNH RHHTT\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

1 ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC  
 51 CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT  
 101 TGAGCCACGC CGTCTGCCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC  
 151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGAG GCATGCTGAT  
 201 GGCACCTGCT GCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG  
 251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCCTC  
 301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC  
 351 TGTAATTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA  
 401 GCCTCACGCT CATTACCCTT GCCGTCATCT ACCGCCCCGT CGTACTCGAA  
 451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GGCGGCAAG GCGGGCTTTG  
 501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC  
 551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT  
 601 ACCGCCCCGC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT  
 651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA  
 701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT  
 751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

1 MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG  
 51 LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL  
 101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTITL AVIYRPLVLE  
 151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGILM SVGLMLPAI  
 201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY  
 251 LFSVILGKEG GILT..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

	10	20	30	40	50	60
m281.pep	MRYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG	LSLPAMGLGG
	:	:	:	:	:	:
g281	MHYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG	LSLPAMGVGG
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALL	AGLVSRFTTL	KEDANFAAFY	LSSLAIGVVL	VSKNGSSVDL	LHLLFGSVLA
	:	:	:	:	:	:
g281	FAAGMLMALL	AGLVSRFTTL	KEDANFAAFY	LSSLAIGVIL	ISKNGSSVDL	LHLLFGSVLA
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIA	AVSSLTITL	AVIYRPLVLE	SIDPLFLKSV	GKGGLWHVL	FLVLVVMNLV

```

g281      |||||:::||:|||||
          VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGGLWHVIFLIILVMNLV
              130           140           150           160           170           180

                190           200           210           220           230           240
m281.pep  SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTAALLCGLSGLLLISYHIEIPSGP
          |||||:::||:|||||
g281      SGFQALGILMSVGIMMLPAITARLWARNMGTLLILLSVLIALFCGLIGLLISYHIEIPSGP
              190           200           210           220           230           240

                250           260
m281.pep  AIIILCCSVLYLFVSILGKEGGILT
          |||||:::||:|||||
g281      AIIILCCSVLYLFVSILGKEGGILPKWFKNHRHHTTX
              250           260           270

```

```

a281.seq
1      ATGCGCTACG  CCTCGCATC  CGTCTTCTGC  CTGTCCCTCA  GTGCCGCACC
51     CGTCGGCGTA  TTCCTCGTCA  TGCGCCGTAT  GAGCCTGATA  GGGCAGCGAT
101    TGAGCCACGC   CGTCTGCC   GGTGCCGCCG  TCGGCTACAT  GTTTGGCCGG
151    TTAAGCCTGC   CGCGCATGG  TTTGGGCGCG  GTAGCCCGAG  GTATGCTGAT
201    GGCATCTGTT   GCGGACTCG  TTGCGCGGTT  CACCACCGTG  AAAGAAGATG
251    CCAACTTTGC   CGCCTTTTAT  CTCAGCAGCC  TCGGCATCGG  TGTAGTCTCT
301    GTCAGCAAAA   ACGGCAGCAG  CGTCGATTTG  CTCACCTCC   TTTTCGGCTC
351    CGTATCTGCC   GTCGATATTC  CTGCCCTGCA  ACTCATCGCC  GCCGTATCCA
401    CCTCACACTG   GCTTACCGTT  GCGGTCATCT  ACCGCCCGCT  CGTACTCGAA
451    AGCATCGACC   CCCTGTTTCT  CAAATCTGTC  GGCGGCAAAG  GCGGGCTTTG
501    GCACGTCCTC   TTTCTCGTCC  TAGTTCGTCAT  GAACCTCGTA  TCCGGCTTTC
551    AAGCCCTCGG   CACATCTAGT  TCCGTCGGAC  TTATGATGCT  CGCAGGCATT
601    ACCGCCCGCC   TATGGGCGAA  GCACATGGGC  GCACTCATCC  TCCTATCCGT
651    TCTGACAGCC   CTGCTGTGCG  GCTTGAGGCG  ACTGCTCATT  TCCTACCACA
701    TCGAAATTCG   TTCGGTCC   GCCATCATCC  TGTGTTGCAG  TCGCTTTTAT
751    CATTTTTCCG   TCATACTCGG  CAAAGAAGGC  GCGATTCTGA  CCAATGGCT
801    CAAAAACCA   CGCCACCACA  CCACCTGA

```

a281. pep  
1 MRYALASVFC LSLSAAPGVG FLVMRRMSLI GDALSHAVLP GAAVGYMFG  
51 LSLPAMGLGG VVAGMIMALL AGLVSRTTTL KEDANFAAFY LSSLAIGVVL  
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSTLTLLTL AVIYRPLVLE  
151 SIDPLFLKSV GKGKGLWHVL FLVLVVMNLV SGFQALGTLM SVGLMLLPAI  
201 TARLWAKHMG ALILLSVLTA LLCLSGLLI SYHIEIPSPG AIILCCSVLY  
251 LFSVLKKEG GILTKWLKNH RHHTT\*

a281	99.2% Identity in 204 aa overlap									
	10	20	30	40	50	60				
m281.pep	MRYALASVFCLSLSAAPVGVLV	MRMRMSLIGDALSHAVLP	GAAVG	YMFAGLSLP	PAMGLGG					
a281	MRYALASVFCLSLSAAPVGVLV	MRMRMSLIGDALSHAVLP	GAAVG	YMFAGLSLP	PAMGLGG					
	10	20	30	40	50	60				
	70	80	90	100	110	120				
m281.pep	VAAGMLMALLAGLVSR	ETTLKEDANFAAFYLS	SLAIGVVLVSKNGSS	VDLLHLLFGSVLA						
a281	VAAGMLMALLAGLVSR	ETTLKEDANFAAFYLS	SLAIGVVLVSKNGSS	VDLLHLLFGSVLA						
	70	80	90	100	110	120				
	130	140	150	160	170	180				
m281.pep	VDIPALQLIAAVSS	LTLLTAVIYRPLV	LESIDPLFLKSVGG	KGGLWHVFLVLV	VVMNLV					
a281	VDIPALQLIAAVST	LTLLTAVIYRPLV	LESIDPLFLKSVGG	KGGLWHVFLVLV	VVMNLV					
	130	140	150	160	170	180				

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

```

g282.seq
1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgc
51  gatcaatccg tttagcgcgt tgctgcctta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgata ggcggtgctg tattgaaggt
201 tttgggcata agcgtcgggt cgtttcaggt cggcggcggtg attttgggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa ggcgcgcccg cccgcaatgc
351 agggcgatt gccgtcgtgc ccacgccat accgatcacc atcggtcggg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcg tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgcg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

```

g282.pep
1  MGLGMEIGKL IVALVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYT
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

```

m282.seq
1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CCGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCGG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CCGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GCGCGACGG
551 GGCTGACGAT TTAAACCGC ATTATGGGTA TGATGCTGGC GCGCGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

```

m282.pep
1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng)

from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	:					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

1	ATGGGATTGG	GCATGGAAAT	CGGCAAGCTG	ATTGTGGCTT	TTTTGGTGCT
51	GATTAATCCG	TTAGCGCGT	TGTCGCTTA	CCTTGACCTG	ACCAACGGGC
101	ACAGCACGAA	GGAGCGCAGG	AAGGTCGCGC	GGACGGCCGC	CGTTGCCGTG
151	TTTGCCGTGA	TTGCGGTATT	TGCGCTGATC	GGCGGTACGC	TGCTGAAGGT
201	TTTGGGCATC	AGCGTCGGTT	CGTTTCAGGT	CGGCGGCGGA	ATTTGGTGT
251	TGCTGATTGC	CATTTCGATG	ATGAACGGCA	ACGACAATCC	CGCCAAGCAG
301	AATCTCGGCG	CGCAGCCGGA	AACGGGGCAG	GTGCGCCCCG	CCGCAATGC
351	CGGAGCGATT	GCCGTCGTGC	CCATCGCCAT	ACCGATCACC	ATCGGCCCGG
401	GCGGTATTTC	GACCGTGATT	ATTTACGCTT	CGGCGGCTAA	AACATACGGC
451	GACATCGCGT	TGATTATCGC	GGCCGGTTTG	GTGGTCAGTG	CGATTGTGTA
501	TGCCATTTTA	ATCGTTGCCG	GGAAGGTCAG	CCGCCTGCTG	GGTGCGACGG
551	GGCTGACGAT	TTTAAACCGT	ATCATGGGTA	TGATGCTGGC	GGCGGTATCG
601	GTGGAGATTA	TTGTGTCGGG	ACTGAAAATG	ATATTCCCGC	AACTGGCAGG
651	TTGA				

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

1	MGLGMEIGKL	IVAFLVLINP	FSALSPLYDL	TNGHSTKERR	KVARTAAVAV
51	FAVIAVFALI	GGTLLKVLGI	SVGSFQVGGG	ILVLLIAISM	MNGNDNPAKQ
101	NLGAQPETGQ	VRPARNAGAI	AVVPIAIPIT	IGPGGISTVI	IYASAAKTYG
151	DIALIIAAGL	VVSAICYAIL	IVAGKVSRL	GATGLTILNR	IMGMLAAVS
201	VEIIVSGLKM	IFPQLAG*			

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282.pep	GATGLTILNRIMGMMLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1  atgaactttg ctttatccgt catcacattt accctcgctt ctttcctgcc
51  cgtcccgctt gccggaaccg ccgtctttac ttggaagac ggcggcggca
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaacg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacg gcagcttgag gaagaaaaga aaaaattgc cgaaccgaa
301 cggcagaaca aagaagaaa ctgccggatt tcaaaaatga acctgaagcg
351 ggtgggaaac tcaaatgcga aaacaagga tgatttgatc cgtaaataca
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1  MNFALSVITE TLASFLPVPP AGTAVFTWKD GGGNSYSVDP KQLHPDQSQI
51  LNLRTLQTKP AVKPKPAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1  ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTG GGATGTACCG AACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGC CGGATTTCAA AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1  MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSVDP KQLHPDQSQI
51  LNLRTLQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRTLQTKP					
	:       :       :       :       :       :					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
		:	:	:	:	:
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNYCRYX					
g283	GNSNAKNKDDLIRKYNNNAVNYCRYX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1173>:

```

a283.seq
1  ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCAGCA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGCG CGGATTTCAG AAATGAACCT
351 GAAAGCGGTG GGAATTTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1174; ORF 283.a>:

```

a283.pep
1  MNFALSVIML TLASFPLVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTQTKP AVKPAQADAG KRTDGAQEN NPDTAEKNRQ LEEKKRIAE
101 TERQNKEENC RISKMNLIKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

m283/a283 100.0% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFPLVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTQTKP					
a283	MNFALSVIMLTLASFPLVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
a283	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRIKMNLIKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNYCRYX					
a283	GNSNAKNKDDLIRKYNNNAVNYCRYX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1175>:

```

g284.seq.
1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51  aggttggggc ttagcggtct ttgtaacggc attcgctttt gcctgcaaaa
101 gagtcgccgg ctttgcggtt gcctttgaag ccttcgccgg tttttttgaa
151 actgtcttct ttaaagcctt ctttcttgaa accttcgccg cgcgttttgc
201 cgccgaagcc ttctttgccc ggtttatgat cgccgcgcgc gccgcgggat
251 ttcctatcgc ccagccgcgc ttgcctttc ggcttgccgc ctgcggattt
301 gcgtttgcgc gccggctcca tgccttcgat ggtcagttcg gccagtttgc
351 ggттаатgта tttttcgatt ttgtggactt tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgc tgcgccgat
451 gcggtggacg tagtcttccg cctgtttcgc caggtcgtag tttatgacgt

```

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```

501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaatcc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggcggcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttggtgga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgcagg atgtggtcga gcaggcggtt
751 tttgtggcgc atatcgtcgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcttt ggtcagtttt
851 cgcgccagtt tgccgactgc gccgtcccaa gtggcggaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51  TVFLKAFFLE TFAARFAAEA FFARFMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFLFR QVVVDVNGG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHFRFG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LLFDLALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1  ATGCCGTCTG AAACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTGTGAA
151 ACCGTCTCTC TTAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTGC
201 CGCCGAAGCC TTCTTGTCTC GGTTCATGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGGCG GTCGGTTCCTA TGCCTTCGAT GGTCACTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TGCGCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TGCGGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGA CGTGAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA CGAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCACTTTC
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTTGCATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGCCCTTT GCCCGGTTTT TCGCTGCGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51  TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFLFR QVVVDVNGG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFGR RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTEKINFA ALHQVHQATAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap



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	10	20	30	40	50	60
m284 . pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAPAGFPAPAAFAFRLAACGFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDFVHFVHGKRNTRACAAGAPDAVDVVFRLFRQVVVDVNGRNVDTACGNI					
g284	FFDFVDFDFVHFVHGKRNTRACAAGAPDAVDVVFRLFRQVVVDVNGRNVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHREFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTKINFALHQVHQTARRGDNQIDREA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1  ATGCCGCTCTG AAACCTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTITTTGAA
151 ACCGTCTCTC TTAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTTTATGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCCTTC GGCTTGCCGC CTGCGGATT
301 GCGTTTGC GGTCGGTTCCA TGCCTTCGAT GGTCAGTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TGCGCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACGTC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT GCGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT GCGCGCGAAA CCTTTTTCGT
651 ACAATTCATC CGCGATGACT TCGGTCATGG CTTTGGTGGA CGTGAAAATC
701 ACGCATTGAT CGATGTCGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GGTCGTCCAC GCGTTCGACT TCGATGATT CAGGTCCTTT GGTGAGTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCT TCCGGCGTGG CTTGACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAG
1001 CGGGCGAAAT CGACTTTGCC GCTTTGCATC AAGTCCATCA GACGGCCCGG
1051 CGTGCGGACA ATCAGATCGA CCGGTTTGCT CAGGGCGCGG GTTTGGTAGC
1101 CGAACGATGC ACCACCGACG ATGCTGACGG TACGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA ATTCGCGGGT
1201 CGGCGTCAAC ACCAACGCGC GCGGGCCTTT GCCCGGTTTT TCGCTGCGTT
1251 TGCTCAGTCG CTGCAAAGTC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE

```

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```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFFDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNO HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDREA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
a284	TFAARFAAEAFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLEFQVVVDNVGNGRYVDTACGNI					
a284	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLEFQVVVDNVGNGRYVDTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAAFQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAAFQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNHQFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSARAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

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g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgccc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

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151  tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201  gtaccaaata cctgctcgtt tcggcgtaaa catttcctcc caaaacctca
251  aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301  gagggggcag accttaaaat cagccgcttc cgcttcgcgt ggaaccgctc
351  cgaactgatg cgcgcgagcc tgcacatcac cgacatctcc gccggcgaca
401  tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451  ggcctgcccc acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501  cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaaccgtct
551  atctcgaacg cctcaacgcg gcataccggt acgaccgtaa agggcaccgc
601  ctcgacctga aggcgcgcga cagcccggtg agcagttcgt cggggtcagc
651  ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701  aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcggc
751  agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801  cctctcgga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851  cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901  gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgccatccc
951  gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttggaaaaa
1001 ccaaagcccg ctttgccgac cgcaacggca tccccgtccg tcagggtttg
1051 ggcggccttg tcatccggca ggacggcacg gtgcatacgc gcaatacgtc
1101 cgccgccctg ctcggacggg cgggcatcag gctgtcgggc aaaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacgcg gttcaaaagg aggttgagcg gcagcatcgg
1251 catcggcgcc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg
1301 gcacggcacg cagggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtgtt cgacaccgtc aacatctccg ccggggaagg
1401 cagcctgacg gcgcaaggct atctcgagct gtttaaagac cgcctgctca
1451 agctgggacat ccgttccgcg gcattcgacc cttcgcgcgt cgatccgcaa
1501 tttccggcag gcaatatcaa cgttccgatt catcttgccg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt tttgcccggt acgttcaacg
1601 gcgtgcccgt tgccggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcgcgc ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
1701 cggcggtctc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgattttatc ccgttccggt ttcggactcg cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggcaaaagc gcagacatcc
1901 gttcgtctga ttttaccctc aaaggctcac ccggcacaag ccgcccgatg
1951 cgcgccgata tcaaggcgcg ccgcctttcc ctgtcgggcg gcgcggcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcgcg cagcaccgca
2051 tccgcacaca cgccgccatg acgctggacg gcaaacggtt caaactcgat
2101 ttggacgctt caggcggcgt caacagggaa cttaccgcat ggaaaggcag
2151 catcggcatc ctcgacatcg gcggcgcatc caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaagc tgcggaacat
2251 tggcaggcaa tggcgcgag cctcaacctg caaacctttt cttgggacag
2301 gaaaaccggc atatcggaac aaggcgcgcg acggcgcgct cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccctcg aacacaatct ggttttaaac
2401 ggcgactggg atgtgcgcta cgggcacaa gcgcgcggct acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttggggt
2501 tgaacgcatt ttccctgaaa acgcgctttc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcggacgg attaacgcgg atttgggcat
2601 cggcaacgcc ttcggcgga atatggcaaa tacaccgctc ggcggcagga
2651 ttacagcctc ctttcccgac ttggcgcat tgaagccctt tctgcccgcc
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcgcgcg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaaa caacggcaat atcacgctcg ggcaaaagcc ctccttcgat
2851 accgcacctt tggcgcgag gctcaacctg accgttgccg atgccaagc
2901 attccgcaac ttcctaccgg tcggacaaaac cgtcaaaagg agcctgaatg
2951 ccgcgtaac cctcgcgggc agcatcgccg acccgcaact gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgctgcgtt cgcatattgc aggcaggaaa tgggtaatcg
3101 agagcctgaa attccggcac gaaggagcgg cggaactctc cggcacggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcggcgcgg tgttcgacaa
3201 ataccgcatc ctgtcccgcc ccaaccggcg cctgacggtt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgatc agggcggtgt cggttcgcaa aaatcctcga tgccgtccgt
3351 agcgacgat gtcgtcgat tggcggaagt caagaaagag gcggcgcatc
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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3451 ttctccggct acggcgcgga cgttaccata ggccggcaaac tgaccctgac
3501 cgccgaaccg ggccggaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aagggcggtt caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgcgga
3651 acgcccgcct tcccccgctg gtgcgggctg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcggca gcagcggcga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccggttc tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

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This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
1   MTDTPPTD TD PTENGTRKMP SEHRPAPPK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RSLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLFA AVYLDRFETG KISMGTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGS LD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIIGIG TTASPKISWQ LGTGARTD G SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRS R AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDL DGG IRTFETDL S G TARNLHIGKA ADIRSLDFTL KGSFPGTSRPM
651 RADIKGGRLS LSGGA AVVD T AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKGSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAA N
751 WQAMGGS LNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFHNLVLN
801 GDWDVAYGHN ARGYNISRQ SGDAVLP GGQ ALGLNAFSLK TRFQNDRI G
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSR SFD
951 TAPLGRLNL TVADAEAFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGG S
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAE LSGTV
1051 SMENSVPD VD IGAVFDKYRI LSRPNRRLTV SGNTRLRYS P QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADV TI GGKLT LTAQP GGNVRGVGT V RVIKGRYKAY GQDL DITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEFMSEK D
1251 KLSWLILNRA GSGSSGD NAA LSAAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLF GSDKK DSAGNGKGK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

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m285.seq
1   ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTGCGCG GCACTGCTGT CTGTCTGTAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CCGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCTCTC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGCGAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAATGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
901 GTGCCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGA AAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGGTTTTA
1051 GCGGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAT CTCTTGCGAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCEG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTCCCGC GCATTGACC CTTCGCGCAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTGCGG GCGAACTGGC
1551 AAAAGAGAAA TTACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTTCGATT GCGGCTGGGG CGGAACATTA TTA AAACAGA
1701 CCGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAC
1751 CCGATTTATC CCGTTTCGGT TTCGGAATCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTG GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CTTTCCGGC GCGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCAGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTGCGGGC GAGCGGCGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCACA
2051 TCGCACACA CGCCGCCATG ACGCTGGATG GCAAAACGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCTTCG AACACAATCT GGTTTTAAAC
2401 GCGGACTGGG ATGTGCGCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGCGGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCCG ATTTGGGCAT
2601 CGCCAAACGCC TTCGGCGGCA ATATGGCAAA TGCACCGCTC GGCGGCAGGA
2651 TTACCGCCTC CTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 CCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAAA CAACGGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCGGCAC GAAGGGACGG CGGAACCTCT CCGTACGGTC
3151 GGATGGA AAAACAGCGACC CGATGTCGAT ATCGGCGCGG TGTTGACAAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGATC AGGGGCTGTT CGGTTGCAA AAATCCTCGA TGCCGTCGCT
3351 CGGCGACGAT GTCGTGCTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC
3451 TTGCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCTGAC
3501 CGCCCAATCG GCGGAAGCG TACGGGCGT GGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCAG
3601 GTCTCCTTTG TCGGCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAATATTTG GGCAGCCTCA
3701 ACAGCCCGCG CATTACGCTG ACGGCAAACG AACCGATGAG TGA AAAAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACGCGGCC GGCAGCGCA GCAGCGCGA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAATCA
3851 ACGACCGCAT CGGGCTGGTG GATGATTG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACGGCGCA ACTCAACCCC GCCGAACAGG TGCTGACCGT
3951 CGGCAAAACA CTGACCGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTGATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCGTTTCG TCGGCGGCG AGCTGACATA

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4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG  
4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep  
1 MDTAPTDT PTENGTRKMP SEHRPTPAK KRRPLLKLSA ALLSVLILAV  
51 CFLGWLAGE AGLRFLYQI PSWFGVNIS QNLKGTLLDG FDGDNWSIET  
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL  
151 SLPDSIDLPA AVYLDRFETG KISMGAFFDK QTVYLERLDA SYRYDRKGHR  
201 LDLKAADTFW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG  
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF  
301 VPSLPDAGLN FDLTAIPFSF DGIALEGS LD LENTKAGFAD RINGIPVRQVL  
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA  
401 EDVLQTAFFK RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN  
451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ  
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TENGVPPIAGS ADIVYESRHL  
551 PRAAVDLRLG RNIKTDDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR  
601 GHLSGDLDDG IRTFETDLSG AARNLHICKA ADIRSLDFTL KGSPDTSRPI  
651 RADIKGSRLS LSGGAHVVDV ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD  
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN  
751 WQAMGGSLNL QHFWDKKTG ISAKGGAHGL HIAELHNFFK PPFENHLVLN  
801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI  
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA  
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSD  
951 TAPLGRLNL TVADAEVFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGG  
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV  
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI  
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR  
1151 FAGYGADVTI GKKLTLLTAQS GGSVRGVGTV RVIKGRYKAY QQDLDTKGT  
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKD  
1251 KLSWLILNRA GSGSSGDNA LSAAAGALLA GQINDRIGLV DDLGFTSKRS  
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI  
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTPTENGTRKMPSEHRPTPAKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTTPTDTPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGTE					
	10	20	30	40	50	60
m285.pep	AGLRFLYQIPSWFGVNISQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
g285	AGLRFLYQIPSWFGVNISQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMGAFFDK					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMGTGFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTFWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAYRYDRKGHRDLKAADTFWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
g285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300



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|||||:|||||
g285 AAQNITGSLNASAIQIGRVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
      910      920      930      940      950      960

      970      980      990      1000     1010     1020
m285.pep TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSSINGDKLYYRNQTQGIILDNG
      |||||:|||||
g285 TVADAEAFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSSINGDKLYYRNQTQGIILDNG
      970      980      990      1000     1010     1020

      1030     1040     1050     1060     1070     1080
m285.pep SLRSHIAGRKVVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
      |||||:|||||
g285 SLRSHIAGRKVVIDSLKFRHEGTAELSGTVSMENSVPDVDIGAVFDKYRILSRPNRRLTV
      1030     1040     1050     1060     1070     1080

      1090     1100     1110     1120     1130     1140
m285.pep SGNTRLRYSPQKGISVTGMIKTDQGLFGSQSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
      |||||:|||||
g285 SGNTRLRYSPQKGISVTGMIKTDQGLFGSQSSMPVSGDDVVVLGEVKKEAAASLPVNMN
      1090     1100     1110     1120     1130     1140

      1150     1160     1170     1180     1190     1200
m285.pep LTLDLNDGIRFAGYGADVTIGGKLTLTAAQSGGVRGVGTVRVIKGRYKAYQDLDITKGT
      |||||:|||||
g285 LTLDLNDGIRFSGYGADVTIGGKLTLTAAQPGGNVRGVGTVRVIKGRYKAYQDLDITKGT
      1150     1160     1170     1180     1190     1200

      1210     1220     1230     1240     1250     1260
m285.pep VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
      |||||:|||||
g285 VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
      1210     1220     1230     1240     1250     1260

      1270     1280     1290     1300     1310     1320
m285.pep GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNAQTGELNPAEQVLTVGKQ
      |||||:|||||
g285 GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNAQTGELNPAEQVLTVGKQ
      1270     1280     1290     1300     1310     1320

      1330     1340     1350     1360     1370     1380
m285.pep LTGKLYIGYEYSSIAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
      |||||:|||||
g285 LTGKLYIGYEYGISSIAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
      1330     1340     1350     1360     1370     1380

      1390
m285.pep DSAGNGKGKX
      |||||
g285 DSAGNGKGKX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

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a285.seq
1 ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGCTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGGCTCGC CGGCACGGAA GCGGGTTTC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAACCGTC
351 CGAACTGATG CGCCGACGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAAACG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCGA CACGCCGTGG AGCAGTTCGT CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA  
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC  
751 AGCCTGAAGG ATGTGCGCGC CGAAGTGGCG ATCGACGCGC GCAATATCCG  
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA  
851 CATTGGAAGA AGTACTGGTC AAAGGTTCA ACATCAATCC GTCCGCCTTC  
901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC  
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA  
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCG TCAGGTTTTA  
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAG GTGCATATCG GCAATACGTC  
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA  
1151 CCGAAAAAGA CATCCTCGAT TTAATATAG GCATCAATC CGTCGGCGCG  
1201 GAAGACGTAC TGCAAAACCG GTTCAAAGGC AGGTTGGACG GCAGCATCGG  
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCCAA CTCGGCATCG  
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCCAGCAAC  
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCG CCGGGCAAGG  
1401 CAGCTGACG GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGTCTA  
1451 AGCTGGACAT CCGTTCCCGC GCATTGACG CTTGCGCAT CGATCCGCAA  
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC  
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG  
1601 GCGTACCGAT TGCCGGCAGT GCGGACATTG TTTACGAGTC CCGCCACCTT  
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTTAAACAGA  
1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAGC  
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC  
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA  
1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC  
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA  
1951 CCGCGCGACA TCAAAGGCG CCGCCTTCG CTGTCGGGCG GAGCGGAGGT  
2001 TGTCGATACC GCGGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGC  
2051 TCCGACACCA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT  
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCGAG  
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC  
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAT  
2251 TGGCAGGCAA TGGGCGGCG CCTCAACCTG CAACACTTTT CTTGGGATAA  
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCGG  
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC  
2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGGCGGCT ACCTCAATAT  
2451 CAGCCGCAA AGCGCGCATG CCGTATTGCC CCGCGGCGAG GCTTTGGGTT  
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC  
2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCGG ATTTGGACAT  
2601 CCGCAACGCC TTCGGCGGCA ATATGGCAAA TGCACCGCTC GCGGCGAGGA  
2651 TTACCGCCTC CCTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC  
2701 GCGGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG  
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCG CGTCAACGGC AGCAGCAACT  
2801 ACGGGAAAAAT CAACGGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT  
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT  
2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAGGC AGCCTGAATG  
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCG ATCCGCATT GGGCGGCAGC  
3001 ATCAACGCGC ACAAACCTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT  
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG  
3101 ACAGCCTGAA ATTCGGGCAC GAAGGGACGG CGGAACCTCT CCGTACGGTC  
3151 GGTATGGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAA  
3201 ATACCGCATC CTGTCCCGCC CCAACCGCGC CCGTACGCTT TCCGGCAACA  
3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT  
3301 AAAACGGATC AGGGGCTGTT CGGTTGCGAA AAATCCTCGA TGCCGTCCGT  
3351 CCGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC  
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC  
3451 TTCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCCTGAC  
3501 CGCCCAATCG GCGGGAAGCG TCGGGGCGT GGGCACGGTC CGCGTCATCA  
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGACATTAC CAAAGGCACG  
3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCGCGCGCA  
3651 ACGCCGCTT TCCCCGTCG GTGCGGCGT GGAATATTG GGCAGCTCA  
3701 ACAGTCCGCG CATTACGCTG ACGGCAAACG AACCGATGAG TGA AAAAGAC  
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA  
3801 CAATGCCGCC CTGTCCGCAG CCGCGGCGC GCTGCTTGCC GGGCAATCA  
3851 ACGACCGCAT CCGGCTGGTG GATGATTGG GCTTTACCAG CAAGCGCAGC  
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTG CCCGTATCGG CAGCCGTTTC TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
1  MDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWLAGE AGLRFLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRFETG KISMGAFAFK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFAK RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 QPKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LRPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIIKTGGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVD ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKSIGI LDIGGAFLNK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PFEHNLVLN
801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFLSK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLA
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRFSD
951 TAPLGGRLNL TVADAEVFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTLTQS GGSVRGVGTV RVIKGRYKAY QQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTGVKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKGK*

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m285/a285 99.4% identity in 1389 aa overlap

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          10      20      30      40      50      60
m285.pep  MDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          |||
a285      MDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          10      20      30      40      50      60

          70      80      90      100     110     120
m285.pep  AGLRFLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM
          |||
a285      AGLRFLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRFAWKPSSELM
          70      80      90      100     110     120

          130     140     150     160     170     180
m285.pep  RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMGAFAFK
          |||
a285      RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMGAFAFK
          130     140     150     160     170     180

          190     200     210     220     230     240
m285.pep  QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
          |||
a285      QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m285.pep  TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
          |||

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a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPPAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
m285.pep	310 320 330 340 350 360
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSGFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
a285	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
a285	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDLDDGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
a285	GHLSGDLDDGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGAAVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSIGI
a285	LSGGAEVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGS LNLOHFSWDKKTGISAKGGAHGL
a285	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGS LNLOHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGLTKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAAQIGGRVGSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
a285	AAQNITGSLNAAAQIGGRVGSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN

657

a285	AAQNITGSLNAAAQIGGRVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
	910 920 930 940 950 960
m285.pep	TVADAEVERNFLEPVGQTVKGSLSNAAVTLGGSIADPHLGGSLNGDKLYYRNQTQGIILDNG
a285	TVADAEVERNFLEPVGQTVKGSLSNAAVTLGGSIADPHLGGSLNGDKLYYRNQTQGIILDNG
	970 980 990 1000 1010 1020
m285.pep	SLRSHIAGRKWWIDSLKFERHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
a285	SLRSHIAGRKWWIDSLKFERHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
	1030 1040 1050 1060 1070 1080
m285.pep	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
	1090 1100 1110 1120 1130 1140
m285.pep	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
a285	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
	1150 1160 1170 1180 1190 1200
m285.pep	VSVFGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIINRA
a285	VSVFGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLIINRA
	1210 1220 1230 1240 1250 1260
m285.pep	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
a285	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
	1270 1280 1290 1300 1310 1320
m285.pep	LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
a285	LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
	1330 1340 1350 1360 1370 1380
m285.pep	DSAGNGKGKX
a285	DSAGNSKGKX
	1390

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

```

1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACATGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAC CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCGACA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAACAACAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGCGCGAAC TGACGATCGA CCGCGGCAAT ATCCGCTCT
701 CCGGAAAAATC CGTCATCCAC CCGTTGCGG AATCATTGGA TAAACATTG
751 GAAGAAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTGGA CCTGACCGCC ATCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCGGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTGGGCGG
951 CTTTGTGATC CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGTCTCG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTAA TATAGGCATC AACTCGTCG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGACAGG ACGGCAGCCT cgcCATCGCA AGCGAcCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTGACA CCGTCAACAT CTCGCGCGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCTTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCTCT TGCCGTGAA CTGGCAAAA
1451 AGAAATTAC GGGCAAAATG CGTTTTTTCG CCGGTACGTT CAACGCGCTG
1501 CCGATTGCGG GCAGCGCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 GCGCGCGCTC GATTGCGGT TGGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCG ACTCGCGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGG GATTGAGCG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTTCG
1801 CTCGATTTTA CCTCAAAGG CTCACCGCGC ACAAGCGGCC CGATGCGCGC
1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTCG
1901 ATACCGCGCG CCTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGACGCAAA CCGTTCAAAC TCGATTGGA
2001 CGCTTCAGG GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGCGGCG GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAA
2201 CCGGCATATC GGCAAAAGGC GCGCGACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CCGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCGGTA TTGCCCCGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGCATCG GAATCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAATACAC CGCTCGCGCG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCGCGCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CCGCAAAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCGCGCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCTC TCGATACGGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATCGCGCC
2851 GTAACCTCG GCGGCAGCAT CGCGACCGCG CACTTGGGCG GCAGTATCAA
2901 CCGCGACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCGCT ATTGCAGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGCGGGAA CTCTCCGGCA CGGTACGCTC
3051 GGAACACAGC GTGCCGATG TCGATATCGG CCGGTTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CCGTTTCCGG CAACACCGCG
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAARAC
3201 TGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTAGACCTC AATGACGGCA TCCGTTCTC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCAGGCGG AAATGTGCGT GGGGTGGGCA CCGTCCGCGT CATCAAAGG
3451 CGTTACAAAG CATAAGGGCA GGATTAGAC ATTACCAAG GCACAGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAACCT GAACATCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGGC GCGGTGGAAA TATTGGGCGC CCTCAACAGC
3601 CCGCGCATTG CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACC GTGCCGGCAG CCGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCGGCA GCGCGCTGCG TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCGCAA
3801 CGCGCAAAAC GCGGAACTCA ACCCGCGCGA ACAGGTGCTG ACCGTGCGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTTACCGG CTGACCGCGC CCATACAGG
3951 GGTGCGCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCCA CCGCCTCTC GGTTCGGACA AAAAAGACTC CGCAGGAAAC
4051 GGCAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:  
g285-1.pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAARYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGLAIA SDPANEORKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAG LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSPG TSRPMRADIK GGRSLSLGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTFRFN DRIGILLDGG ARFGRINADL GIGNAFGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNASAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVQG SRSFDTAPLG GRNLNTVADA EAFRNLFPVG QTVKGSLNAA
951 VTLGGSIAPI HLGGSSINGDK LYRNRQTQGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAASL
1101 PYNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIKG
1151 RYKAYGQDL ITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACCTGCTCGC ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAATAC CGTCATCCAC CCGTTTCCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCG GATGCCGGAC TGAATTCGTA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGTTCCG TCGATTGGA AAACACCAA
901 GCCGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGCGGG
951 CTTTGTGATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCTTGCTCGG ACGGGCGGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAT TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTCGAA ACCCGGTTC AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACGCGCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATTT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCCGTC GATTGCGGC TGGGGCGGAA CATTATTAAT ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGT GATTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGCGGCAGC CATCCGTTCC
1801 CTCGATTTCA CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTGC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGG CCAATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGCGC GATTCAACCC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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660

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CGGGCATATC GGCAAAAGGC GGCACACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
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2451 TGACGGCGGC GCGCGTTTCG GCGGATTAA CGCCGATTG GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTCTGCG CCGCCGCCCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCG CGCGCAAATC GCGGACGGG
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2901 CGGCGACAAA CTCTATTACC GCAACCAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT CGGTCGCAT ATCGCGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGCGGAA CTCTCCGTA CGGTCGGTAT
3051 GGAAGACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CGCCGCTGA CGGTTCCGG CAACACCCCG
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGG GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGTGGGCA CGGTCGCGT CATCAAAGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAG GCACGGTCTC
3501 CTTTGTGGCG CGGCTCAACG ATCCCAACCT CAACATCCG GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGGG GCGGTGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTG CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGGCTC ATCTCAACC GCGCCGGCAG CGGCAGCAGC GGCACAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTT ACCAGCAAGC GCAGCCGCAA
3801 CGGCAAAACC GCGCAACTCA ACCCCGCCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 CGGGAACAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAGACTC CGCCGAAAC
4051 GGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTFPKE ERPPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGNN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDNLIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLSLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLG DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPP TSRPIRADIK GSRLSLSGGA AVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRT
851 ASLPDLGALK PFLPAAQNI TGSLNAAQI GGRVGSFSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRLNLTVADA EVFRNPLPVG QTVKGSLNAA
951 VTLGGSIAFP HLGGSSINGDK LYRNTQOGI ILDNGLSRSH IAGRWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PYNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSRV GVGTVRVIKG
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSFVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRDFRS GSDKKDSAGN
1351 GK GK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

661

g285-1.pep	LKLSAALLSVLILAVCFLGWIAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDN
m285-1	LKLSAALLSVLILAVCFLGWLAGEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDN
	10 20 30 40 50 60
	70 80 90 100 110 120
g285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPPLSLPDS
	70 80 90 100 110 120
	130 140 150 160 170 180
g285-1.pep	IDLPAAYLDRFETGKISMGKTFDKQTVYLERLNAAYRYDRKGHRLDLKAADTPWSSSSG
m285-1	IDLPAAYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG
	130 140 150 160 170 180
	190 200 210 220 230 240
g285-1.pep	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRaelTIDGgnIRLSGKSVIH
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRaelaIDGgnIRLSGKSVIH
	190 200 210 220 230 240
	250 260 270 280 290 300
g285-1.pep	PFAESLDKTLLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
m285-1	PFAESLDKTLLEEVLVKGFNINPAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
	250 260 270 280 290 300
	310 320 330 340 350 360
g285-1.pep	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAAALLGRGGIRLSGKIDTEKDILDLNIGI
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAAALLGRGGIRLSGKIDTEKDILDLNIGI
	310 320 330 340 350 360
	370 380 390 400 410 420
g285-1.pep	NSVGAEDVLQTAfKGRldGSIGIGTTASPKISWQLGTGTARTDGSlaIASDPANEQRKL
m285-1	NSVGAEDVLQTAfKGRldGSIGIGTTASPKISWQLGIGTARTDGSlaIASDPANGQRKL
	370 380 390 400 410 420
	430 440 450 460 470 480
g285-1.pep	VFDTVNISAGEGSLTAQGYLEfKDRllKldIRsRAfDPSRIDPQfPAGDINGSIHLAGE
m285-1	VLDTVNIaAGQGSLSLAQGYLEfKDRllKldIRsRAfDPSRIDPQLPAGNINGSINLAGE
	430 440 450 460 470 480
	490 500 510 520 530 540
g285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD
	490 500 510 520 530 540
	550 560 570 580 590 600
g285-1.pep	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTfETDLsGTARNLHIGKAADIRS
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTfETDLsGAARNLHIGKAADIRS
	550 560 570 580 590 600
	610 620 630 640 650 660
g285-1.pep	LDFTLKGSPTSRPMRADIKGGRSLSLSGGAaVVDTAGLTLEGTGAQHRIrTHaAMTLDGK
m285-1	LDFTLKGSPTSRPIRADIKGSRSLSLSGGAaVVDTADLMDGTGVQHRIrTHaAMTLDGK
	610 620 630 640 650 660
	670 680 690 700 710 720
g285-1.pep	PFKLDLDASGGINRELTRWKGSIGILDIGGAfNLKLQNRMTLEAGAEHVAASaANWQAMG
m285-1	PFKFDLDASGGINRELTRWKGSIGILDIGGAfNLKLQNRMTLEAGAErVAASaANWQAMG
	670 680 690 700 710 720
	730 740 750 760 770 780
g285-1.pep	GSLNLQHfSWDRKtGISAKGGAGLHIAELHNfFKPPfEHNlVLNGDWDVAYGHnARGYL
m285-1	GSLNLQHfSWDKKtGISAKGGAGLHIAELHNfFKPPfEHNlVLNGDWDVAYGRnARGYL



662

	730	740	750	760	770	780
g285-1.pep	790	800	810	820	830	840
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
g285-1.pep	850	860	870	880	890	900
m285-1	ANTPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSVNAAVNGSSNYG					
	850	860	870	880	890	900
g285-1.pep	910	920	930	940	950	960
m285-1	KINGNITVGQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLSNAAVTLGGSIAADP					
	910	920	930	940	950	960
g285-1.pep	970	980	990	1000	1010	1020
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVMENS					
	970	980	990	1000	1010	1020
g285-1.pep	1030	1040	1050	1060	1070	1080
m285-1	VPDVGAVFDKYLRLSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
g285-1.pep	1090	1100	1110	1120	1130	1140
m285-1	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVITGGKLTTLTAQPGGNVR					
	1090	1100	1110	1120	1130	1140
g285-1.pep	1150	1160	1170	1180	1190	1200
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLIRAEERLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
g285-1.pep	1210	1220	1230	1240	1250	1260
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
g285-1.pep	1270	1280	1290	1300	1310	1320
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
g285-1.pep	1330	1340	1350			
m285-1	IGSRSSGGELTYTIRFDRFSGDDKDSAGNGKGK					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1 CTGAAGCTGT CGGCGGCACT GCTGCTGTCT CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG CTCGCCGCGA CGGAAGCGGG TTGCGCTTC GGGCTGTACC
101 AAATCCCTGC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTCCGCGCG CGACATCGCC
301 ATCGTTACCA AACCAGACTCC GCCTAAAGAA GAACGCGCG CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAGGC
601 GGAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAATAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCG GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 CCGCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAAG TTTTAGGCAG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG CGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
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1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCGATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTC GATTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGC GATTGAGCG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCCGCCGAC ACAAGCCGCC CGATACGGCG
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTCTG
1901 ATACCGCCGA CCTGATGCTG GACGGCAGCG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGGCG GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACACACG GTCTGCATAT CGCCGAGTTG
2251 CACAAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAGGCGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGGATTAAC CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTGCG CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCCG CGCGCAAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCCGCTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG CGCGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCG GGCACGAAGG GACGGCGGAA CTCTCCGTA CCGTCGGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CGGTTTCCGG CAACCCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTTCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAATCAAAA AAGAGCGGCG GGCACCGCTC
3301 CCGCTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGGCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGAGG ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CCGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAT TATTGGGCG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACC GCGCCGGCAG TGGCAGCAGC GCGGACAAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGCT TTGCCGGGCA AATCAACGAC
3751 CCGATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GCGGAACTCA ACCCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACCTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

## a285-1.pep

```

1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLRGGG IRLSGKIDTE
351 KDILDNLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLSLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS-
601 LDTPLKGSPP TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFETKPFEP NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILDGG AREGRINADL DIGNAFGGNM ANAPLGGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSNLAAQI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLTVADA EVFRNFLPVG QTVKGSNLAA
951 VTLLGSIADP HLGGSINGDK LYRNQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVE DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSGR GVGTVRVIKG
1151 RYKAYGQDLD ITRGTVSFVG PLNDPNLNR AERRLSPPVA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGVEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRDFRS GSDKKDSAGN
1351 SKGK*

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a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDS					
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
m285-1	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGGGIRLSGKIDTEKDILDNLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGGGIRLSGKIDTEKDILDNLNIGI					
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL					
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	LTAGGYLE	LFKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	INLAGE
m285-1	VLDTVNIAAGQGS	LTAGGYLE	LFKDRLLK	LDIRSR	AFDPSRID	PQLPAGNINGS	INLAGE
	430	440	450	460	470	480	
a285-1.pep	LAKEKFTGKMR	FLPGTFNG	VPIAGSAD	IVYESRHL	PRAAVDL	RRLGRNI	IKTDGGFGKKGD
m285-1	LAKEKFTGKMR	FLPGTFNG	VPIAGSAD	IVYESRHL	PRAAVDL	RRLGRNI	IKTDGGFGKKGD
	490	500	510	520	530	540	
a285-1.pep	RLNLNITAPDL	SRFGFLAG	SLNVRGHL	SGDLGG	IRTFTDL	SGAARNL	HIGKAADIRS
m285-1	RLNLNITAPDL	SRFGFLAG	SLNVRGHL	SGDLGG	IRTFTDL	SGAARNL	HIGKAADIRS
	550	560	570	580	590	600	
a285-1.pep	LDFTLKGS	PDTSRPIR	ADIKGSRL	SLSGGAE	VVDATD	MLDGTG	VQHRIRTHAAMTLDGK
m285-1	LDFTLKGS	PDTSRPIR	ADIKGSRL	SLSGGAE	VVDATD	MLDGTG	VQHRIRTHAAMTLDGK
	610	620	630	640	650	660	
a285-1.pep	PFKFDLDAS	GGINREL	TRWKGSI	GILDIG	GAFNLK	LQNRMT	LEAGAEVAASAANWQAMG
m285-1	PFKFDLDAS	GGINREL	TRWKGSI	GILDIG	GAFNLK	LQNRMT	LEAGAEVAASAANWQAMG
	670	680	690	700	710	720	
a285-1.pep	GSLNLQHFS	WDKKTG	ISAKGGA	HGLHIA	ELHNFF	KPPFEH	NLVLNGDWDVAYGRNARGYL
m285-1	GSLNLQHFS	WDKKTG	ISAKGGA	HGLHIA	ELHNFF	KPPFEH	NLVLNGDWDVAYGRNARGYL
	730	740	750	760	770	780	
a285-1.pep	NISRQSGDA	VLPGGQAL	GLNAFSL	KTRFQND	RIGILLD	GGARFGR	INADLDIGNAFGGNM
m285-1	NISRQSGDA	VLPGGQAL	GLNAFSL	KTRFQND	RIGILLD	GGARFGR	INADLDIGNAFGGNM
	790	800	810	820	830	840	
a285-1.pep	ANAPLGGRI	TASLPDL	GLTKPFL	PAAQNI	TGSLNAA	QIGGRV	GSPSVNAAVNGSSNYG
m285-1	ANAPLGGRI	TASLPDL	GLTKPFL	PAAQNI	TGSLNAA	QIGGRV	GSPSVNAAVNGSSNYG
	850	860	870	880	890	900	
a285-1.pep	KINGNITV	GQSR	SFDTAP	LGGRLN	TVADAE	VFRNFL	PVGQTVKGS
m285-1	KINGNITV	GQSR	SFDTAP	LGGRLN	TVADAE	VFRNFL	PVGQTVKGS
	910	920	930	940	950	960	
a285-1.pep	HLGGSING	DKLYRN	QTQGI	IILDNG	SLRSHI	AGRKWV	IDS
m285-1	HLGGSING	DKLYRN	QTQGI	IILDNG	SLRSHI	AGRKWV	IDS
	970	980	990	1000	1010	1020	
a285-1.pep	GPDVDIG	AVFDKYR	ILSRPN	RRLTVS	GNTRLR	YSPQK	GISVTG
m285-1	GPDVDIG	AVFDKYR	ILSRPN	RRLTVS	GNTRLR	YSPQK	GISVTG
	1030	1040	1050	1060	1070	1080	
a285-1.pep	SVGDDVV	VLGEVK	KEAAAP	LPVNMN	LTLDL	NDGIRF	AGYADV
m285-1	SVGDDVV	VLGEVK	KEAAAP	LPVNMN	LTLDL	NDGIRF	AGYADV
	1090	1100	1110	1120	1130	1140	
a285-1.pep	GVGTVR	VIKGRY	KAYGQD	LDITK	GTVSF	VGPLND	PNLNIRA
m285-1	GVGTVR	VIKGRY	KAYGQD	LDITK	GTVSF	VGPLND	PNLNIRA
	1150	1160	1170	1180	1190	1200	

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKKGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

```

g286.seq
1  atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatatt ttctttccgc acgcatacgc gcctgccgcc gacctttccg
101 aaaacaagc gcggttttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaaacc caaattcccc gtcgcgcatc acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251 agcaggaaga ggttttgat aaggaacaga cgggattcct tgccgaagaa
301 gcaccggaca acgttaaac aatgctccgc agcaaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacgggt cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaaca
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaaggcta cccgcttgcc
601 aagctcggca acaccgggc gccgtcaac cccgataccg ccaccgcca
651 tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcaccgg cacacagcgt taccccaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcatatttc cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgctc cccgtcaaa gtagcgtaac
901 cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggctcg ctgggatatg gacaaatag aaaccacgct
1051 tgccgccggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaacgcgcc
1151 ttctccggcg gcatctggtg tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaaatccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaacgcg
1301 cagctgctca acaacgtgct gcaccccga aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tattttctca cgcgcgaaaa caaaaaactc
1451 ggcacgttca tcatacgcgg acaagcgggt tacaccgttg cgcgcgacaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcgcc gcgtcttccg
1551 tgcgcgggta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

```

g286.pep
1  MONTGTMKIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLKPFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAI LGD
151 ILSGDNLA EY RNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTAAVN PDTATADLNV VDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLDFQAL EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301 RGQTPQTRNR HPPRFGIRFG RQNRLLRLQ LQQRLYRLGR LGYGQIRNHA
351 CRRHQPAQAL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRCQ
401 AGGGISR RRR ENPRLGCRFG QPRHDADRL LETPAAQQA APRKRPLPRR

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667

451 QNRDDFGHIP VLHRANPHLC PRRLFLHARK QKTRHVHHTR TSGLHRCTRQ  
 501 CRCLPGADVQ QRRRVFRARL RT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq  
 1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC  
 51 GGCTTTATTT TTCTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG  
 101 AAAACAAGGC GCGGGTTTC GCATTGTTC AAAACAAAAG CCCCGACACC  
 151 AATCAGTCA AATTAACC CAAATCCCC GTCTCATCG ACACGCAGGA  
 201 CAGTGAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGC  
 251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCTT CGCCGAAGAA  
 301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTGAGCAG  
 351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC  
 401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC  
 451 ATCTTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA  
 501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA  
 551 GCAAAACTTC CGTCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC  
 601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACGCGCGA  
 651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCGACTTTG  
 701 AAATCACCAG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGCG  
 751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA  
 801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCTCC GTACAAGCCG  
 851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC  
 901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCCTCG ATTCGGAATA  
 951 CGGTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG  
 1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT  
 1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CCGGGCAACT ACTGGACAAG  
 1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT  
 1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGCGAT CGATGCCAGG  
 1201 CTGGGGGCGG AATTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT  
 1251 CGATTGGGC AACAGCCAGC CCACGATGCT GACCGCTCT TGGAAACGCC  
 1301 AGCTGCTCAA CAACGTGCTG CATCCGAAA ACGGCCATTA CCTCGACGGC  
 1351 AAAATCGSTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG  
 1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCCGAAAAC AAAAACTCG  
 1451 GCACGTTTCA CACGCGGA CAAGCGGTT ACACCGTTGC CCGCGACAAT  
 1501 GCCGACGTTT CTTAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT  
 1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG  
 1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG  
 1651 TTTACGCGCA CCCTTCCGG CGCGGTGTT CACGATATGG GCGATGCCGC  
 1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC  
 1751 GCTGGTTCAG CCCGCTTGGC CCGTTTCTCT TCGACATCGC CTACGGGCAC  
 1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep  
 1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT  
 51 ESVKLPKFP VLIDTQDSEI KDMVEHLPL ITQQQEEVLD KEQTGFLAEE  
 101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAILED  
 151 ILSDGNLAIE YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA  
 201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA  
 251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDRLQG DRVPVKVSVT  
 301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYSVSV WMDKYETTL  
 351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFGSGVWY VRDRAGIDAR  
 401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG  
 451 KIGTTLGTFLL SSTALIRTS RAGYFTT PEN KKLGTFFIRG QAGYTVARDN  
 501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP  
 551 FTRLTGSAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH  
 601 SDKKIRWHIS LGTRF\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKNK	SPDTESVKCLKPKFP			
g286	MQNTGTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKSK	SPDTESVKCLKPKFP			
	10	20	30	40	50	60
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQ	EEVL DKEQTGLAE	EAPDNVKTMLRSKGYFSSKVS			
g286	VRLDTQDSEIKDMVEEHLPLITQQQ	EEVL DKEQTGLAE	EAPDNVKTMLRSKGYFSSKVS			
	70	80	90	100	110	120
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVA	ILGDI LSDGNLAEYRNAL	ENWQQPVGSDFFQDS			
g286	LTEKDGAYTVHITPGPRTKIANVGVA	ILGDI LSDGNLAEYRNAL	ENWQQPVGSDFFQDS			
	130	140	150	160	170	180
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQA	AVNPD TATADLNVVDSGRPIA	FGDFEITGTQR			
g286	WENSKTSVLGAVTRKGYPLAKLGNTRA	AVNPD TATADLNVVDSGRPIA	FGDFEITGTQR			
	190	200	210	220	230	240
m286.pep	YPEQIVSGLARFQPGMPYDL DLLDFQQA	LEQNGHYS GASVQADFDRL-QGDRV	VPVKVSV			
g286	YPEQTVSGLARFQPGTFYDL DLLDFQQA	LEQNGHYS GASVQADFDRLPRGFR	PRQSRN			
	250	260	270	280	290	299
m286.pep	TEV KRHKLETGIRLDSEYGLGGKI	ADYNYNLFNKGYIGSVVWMDK	YETTLAAGISQPRN			
g286	RGQTPQTRNRHPPRFGIRFGRONRL	LQLQRLYRLGRIGYGQIRNHACRR	HQPAAQL			
	310	320	330	340	350	360

a286.seq

seq	1	ATGCACGACA	CCCGTACCAT	GATGATTAAG	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTCCCG	
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTGTA	AAAAACAAAG	CCCCGACACC	
151	GAATCAGTTA	AATTAATAAC	CAAAATCCCC	GTCCGCATCG	ACACGCAGGA	
201	TAGTGAAATC	AAGAATATGG	TCGAAGAACA	CTCGCCGCTC	ATTACGCAGG	
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA	
301	GCACCGGACA	ACGTTAAATC	AATGCTCCGC	AGCAAAGGCT	ATTTCAGCAG	
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGGAC	TTATACGGTA	CACATCACAC	
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTGC	CGCTCGCCAT	CCTCGCGCAC	
451	ATCCTTTAGC	CGCCAACTC	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA	
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCGA	TCAGGACAGT	TGGGAAAAACA	
551	GCAAACATTC	CGTCTCCGG	CGCGTAAACG	GCAAAGCCTA	CCCGCTTGCC	
601	AAGTCGGCA	ACACCCGGGC	GGCGCTCAAC	CCCGATACCA	CCACCGCCGA	
651	TTTGAACGTC	TCGTGTGACA	CGCGCCGCCC	CATCGCCTTC	GGCGACTTTG	
701	AAATTACCGG	CACGCAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCTTGGCG	
751	CGCTTCCAAC	CGGGCAACGC	CTACGACCTC	GAGCTGTGTC	TGCAGTTCCA	
801	ACAGGCGCTC	GAACAACAGC	GGCATTTATC	CGGCGCGTCC	GTACAAGCCG	
851	ACTTCGACCG	CTCCAAGGCG	GACCGCGTCC	CCGTCAAAGT	CAGCGTAAAC	
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCGCTG	ATTTCGGAAT	
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTACAACAAAG	
1001	GCTATATCCG	TTCCGTCGTC	TGGGATATGG	ACAAATACGA	AACCAACGCT	
1051	GCCGCCGGCA	TACGACGACC	CGCAACTACT	CGGGGCAACT	ACTGGACAAG	
1101	CAACGTTTCC	TCAGACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT	
1151	TCTCCGCGCG	CATCTGGTAT	GTGCGCGACC	GCGGGGGCAT	CGATGCCAGG	
1201	CTGGGGGCGG	AGTTTCTCGC	AGAAGGCCCG	AAAATCCCCG	GCTCGGATAT	
1251	CGATTTTGGC	AACAGCCACG	CCACGATGCT	GACCGCCTTC	TGGAAACGCC	
1301	AGCTGCTCAA	CACGTCGTGC	CATCCCGAAA	ACGGCCATTA	CTCGACGGCG	

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1351 AAAATCGGTA CGACTTTGGG CGCATTCTCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTCAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCC AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTCTCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
1  MHDTRTMMIK PTALLLPALF FFFHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAILED
151 ILSGNNLAIE YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDATADLNV VDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA EQNGHYS GASVQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG KIAIDYNNL FNKGYIGSVV WMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFGGIWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSDIDL NSHATMLTAS WKRQLNNVL HPENGYLDG
451 KIGTTLGAFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLGSAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

m286/a286 98.7% identity in 615 aa overlap

10 20 30 40 50 60
m286.pep MHDTRTMMIKPTALLLPALFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP
|||||
a286 MHDTRTMMIKPTALLLPALFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP
10 20 30 40 50 60

70 80 90 100 110 120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
| |||||
a286 VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
70 80 90 100 110 120

130 140 150 160 170 180
m286.pep LTEKDGYTVHITPGPRTKIANVGVAILGDILSDGNLAIEYRNALENWQQPVGSDFDQDS
|||||
a286 LTEKDGYTVHITPGPRTKIANVGVAILGDILSDGNLAIEYRNALENWQQPVGSDFDQDS
130 140 150 160 170 180

190 200 210 220 230 240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR
|||||
a286 WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR
190 200 210 220 230 240

250 260 270 280 290 300
m286.pep YPEQIVSGLARFQPGMPYDLDLLLDFQQA EQNGHYS GASVQADFRLQGDRVPVKVSVT
|||||
a286 YPEQIVSGLARFQPGTPYDLDLLLDFQQA EQNGHYS GASVQADFRLQGDRVPVKVSVT
250 260 270 280 290 300

310 320 330 340 350 360
m286.pep EVKRHKLETGIRLDSEYGLGGKIAIDYNNL FNKGYIGSVVWMDKYETTLAAGISQPRNY
|||||
a286 EVKRHKLETGIRLDSEYGLGGKIAIDYNNL FNKGYIGSVVWMDKYETTLAAGISQPRNY
310 320 330 340 350 360

370 380 390 400 410 420

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670

m286.pep	RGNYWTSNVSYNRSTQNLEKRAFGSGGVVYVRDRAGIDARLGAFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTQNLEKRAFGSGGIWYVRDRAGIDARLGAFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNPNSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPNSGLMFRSGGASSVRGYELDSIGLAGPNPNSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLLEYQLPFTRTLGSAVFHDMGDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
a286	LVGSLLEYQLPFTRTLGSAVFHDMGDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGRFX
a286	SDKKIRWHISLGRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

```

1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggccgtggcg gatcgcccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggccgcccc gttgttgctg aaaatgccgg ggaagggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcgggt cggaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgcga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgaccacc tgtaaaggcg attcttgtaa tggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtg tgaagaaaa
601 attagcgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttccggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttga
1151 cggaataatg cggcggggat gtttccgga ggttttacg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattccgc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51 LPKEKKDEEA AGGAPQADTQ DATAGEGSDQ MAAVSAENTG NGGAATTDNP
101 KNEDAGAQN DMPQNAESAN QTGNQNPAGS SDSAPASNPA PANGGSDFR

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151 TNVGNVSVID GPSQNLTLH CKGDSNNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGNTKYI IFYTDKPPTR SARSRRSLPA
251 EIPLIPVNOA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVGGIISG DDLHMGTKF KAAIDGNGFK GTWTENGSGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFG VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1 ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTGG CCCTTTCAGC
51 CTGCGGGGGC GCGGGTGGCG GATCGCCCGA TGTCAGTCCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTTCCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAATAACAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GCGGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTGAGATCC CATCCCCGCG TCAAACCTTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGGA GGGTTGATT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGA TGAGAAGTA CAGCTAAAAT CAGAATTGTA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTGCGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCGGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGCGAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATT TTGCGGCAAA TCTGTGGACG GCATTATCGA
1251 CAGCGGCGAT GATTTCGATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAAACGG CTTTAAGGGG ACTTGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMAANA
151 DGMQGDPSA GGQNAAGTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVVDLANG VLIDGPSQNI TLTHCKGDSG SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRSLPAE MPLIPVNQAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDGSK SVDGIIDSGD DLHMGTKQFK AADGNGFKG TWTENGSGDV
451 SGKIFYGPAGE EVAGKYSYR PTDAEKGFGV FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEAK
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKKDEEA
          10      20      30      40      50      60

```

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAAGT						
	:	::					
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNDMPQNAA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDPSAGGQNAAGTA						
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTILTHCKGDS						
	::   :						
g287	-ESANQTGNNQAPAGSSDSAPASNPAPANGGSDFRNTVNGNSVVIDGPSQNTILTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMGKINQYIIFYKP						
	:: :		::		:::		:
g287	CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT						
	:						
g287	KPPT-----RSARSRRSLPAEIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYF						
g287	KSVVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYF						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGFGVFAGKKEQDX						
g287	PTDAEKGFGVFAGKKDRDX						
	420	430					

a287.seq

```
1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51 TGTGTGGGGC GCGGTGGGCG GATCGCCGA TGTTTAGTCG GCGGACACGC
101 CTGCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCGCGAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG
251 TTTCCGCAGA AAATACAGGC AATGCGCGT GCGGCAACAAC GGATAATCCC
301 GAAATAAAGC ACGAGGGACC CAAAAATGAT ATGCCGCAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATTCGGC ACACACGGCA
451 AACCAACCGC ATATGGCAAA TGCGGCGGAG GGAATGCAGG GGGACGATCC
501 GTCGCGAGGG GAAATGCCG GCAATACGCG AGATCAAGTG GCAAAATCAAG
551 CTGAAACCAA TCAAGTCGCG GGCTCTCAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGAG GTTCGGAATA TGTAACGTTG ACACATTGTA
701 AAGACAAAGT ATGCGCATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA
```

a287.pep

1	MFKRSVIAMA	CIVALSACGG	GGGSPDVKS	ADTLSPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAVSAENTG	NGGAATDNP
101	ENKDEGPQND	MPQNAADTDS	STPNHTPAPN	MPTRDMGNQA	PDAGESAPQA
151	NQPDMANAAD	GMQGDPSAG	ANENGTADQA	ANQANNNQVG	GSFNPASSTN
201	PNATMGSSDF	GRINDVANGIK	LDSGSENVTL	THCKDKVCDR	FLDEEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSARFRRSA	RSRRSLPAEM	PLIPVQNAQD	LIVDGEAVSL	TGHSNGTIFAP
351	EGNYRYLTYG	AEKLSGGSYA	LSVQGEPAKG	EMLAGTAVYN	GEVLHFFHMEN
401	GRPSPSGGRF	AAKVDFFGSK	VDGIDSGDD	LHMGTKQKFA	VIDNGNFKGT
451	WTENGGGDVS	GRFYGPAGEE	VAGKYSYRPT	DAEKGFGVF	AGKKEQD*

m287/a287 77.2% identity in 501 aa overlap

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPAAPV	VSSE-----	KETEA		
a287	MFKRSVIAMACIVALSACGGGGGSPDVKSADTLSPAAPV	VTEDVGEEVLPKEKKDEEA			
	10	20	30	40	50
	50	60	70	80	90
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGN	GGAVTADNPFKNEDEVAQN	DMPQNAAGT		
a287	VSGAPQADTQ--DATAGKGGQDMAAVSAENTGN	GAATTDNPFENKDEGPQNDMPQNAADT			
	70	80	90	100	110
	110	120	130	140	150
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQ	PANQPDMANAADGMQGGDPSAGGQ	NAGNTA		
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQ	PANQPDMANAADGMQGGDPSAG--ENAGNTA			
	120	130	140	150	160
	170	180	190	200	210
m287.pep	AQGANQAGNNAAGSSDPIPASNPAPANGGS	NFGRVDLANGVLIDGPSQ	NITLTHCKGDS		
a287	DQAANQAEENNQVGGSQNPASSTPNATNGGS	DFGRINVAINGIKLDSGSENVTLTHCKDKV			
	180	190	200	210	220
	230	240	250	260	270
m287.pep	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKD	GKNDKEVGLVADSVQMKGINQYIIFYKP			
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDE	QRENFVGLVADRVEKNGTNTKYVYIYKD			
	240	250	260	270	280
	290	300	310	320	330
m287.pep	KP--TSFARFRRSARSRSLPAEMPLIPVNQAD	TLIVDGEAVSLTGHSGNIFAPEGNRYR			
a287	KSASSSARFRRSARSRSLPAEMPLIPVNQAD	TLIVDGEAVSLTGHSGNIFAPEGNRYR			
	300	310	320	330	340
	350				

674

	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDDGIIDSGDDLHMGTKQKFAAIDGNGFKGTWTENGSGDVSCKFYGPAGEEVAGKYS					
a287	GSKSVDDGIIDSGDDLHMGTKQKFAVIDGNGFKGTWTENGSGDVSCKFYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggt aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgtcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcggtg cgcccttacc gcaccttttc
201 acccttgctt gtgctgcaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcgcggcgg ttaaccggca ttctaccctg
301 cggagcccg actttcctcc ccgtatgcct tacgcgatac gcgcgactg
351 tctgcccgtc ccgtgtgctg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcctt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPFRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCAGTTTGT CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCGCGCGG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCTCTC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCCTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPFRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

675

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVPCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLVPCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	:     :     :     :     :					
g288	PCAARIITRNTKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180

m288.pep	DTX
	:
g288	DAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTCTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCTT GTGCTGCCAA AGCAGCCATC GCGCGTTTTC CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1210; ORF 288.a&gt;:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVPCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLVPCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	:     :     :     :     :					

a288            PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFVACAQVF  
    130                    140                    150                    160                    170                    180

m288.pep       DTX  
                   ::  
 a288            NAX

-- The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

g290.seq  
 1    atggcaaaaa   tgatgaaatg   ggcggctggt   gcggcggtcg   cggcggcagc  
 51    ggtttggggc   ggatggtctt   atctgaagcc   cgaaccgcag   gctgcttata  
 101   ttacggaagc   ggtcaggcgc   ggcgatatca   gccggacggt   ttccgcgacg  
 151   ggcgagattt   cgcggtccaa   cctggtatcg   gtcggcgcg   aggcttcggg  
 201   gcagattaaa   aagctttatg   tcaaactcgg   gcaacaggtc   aaaaaggcgc  
 251   atttgattgc   ggaaatcaat   tcgaccacgc   agaccaacac   gatcgatatg  
 301   gaaaaatcca   aattggaac   gtatcaggcg   aagctggtgt   ccgcacagat  
 351   tgcatggtgc   agcgcggaaa   aaaaatataa   gcgtcaggcg   gcgttgtgga  
 401   aggatgatgc   gacctctaaa   gaagatttgg   aaagcgcgca   ggatgcgctt  
 451   gccgcccgcca   aagccaatgt   tgccgagttg   aaggctttaa   tcagacagag  
 501   caaaatttcc   atcaataccg   ccgagtcgga   tttgggtac   acgcgcatta  
 551   ccgcgacgat   ggacggcacg   gtggtggcga   ttcccggtga   agaggggcag  
 601   actgtgaacg   cggcgacgac   tacgccgacg   attgtccaat   tggcgaatct  
 651   ggatatgatg   ttgaacaaaa   tgcagattgc   cgaggcgcat   attaccaagg  
 701   tgaaggcggg   gcaggatatt   tcgtttacga   ttttgtccga   accggatacg  
 751   ccgattaagg   cgaagctcga   cagcgtcgac   cccgggtgta   ccacgatgtc  
 801   gtcggggcgc   tacaacagca   gtacggatac   ggcttccaat   gcggtctatt  
 851   attatgcccg   ttcgtttgtg   ccgaatccgg   acggcaaaact   cgccacgggg  
 901   atgacgacgc   agaatacggg   tgaatcgac   ggtgtgaaaa   atgtgttgct  
 951   tattccgtcg   ctgaccgtga   aaaatcggcg   cggcaaggcg   ttcgtacgcg  
 1001   tgttgggtgc   ggacggcaag   gcagtggaac   gcgaaatccg   gaccggatg  
 1051   aaagacagta   tgaataccga   agtgaaaagc   ggggtgaaag   agggggacaa  
 1101   agtgggtcatc   tccgaaataa   ccgccgccga   gcagcaggaa   agcggcgaa  
 1151   gcgccctagg   cggcccgccg   cgccgataa

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

g290.pep  
 1    MAKMMKWAAY   AAVAAAAVWG   GWSYLKPEPQ   AAYITEAVRR   GDISRTVSAT  
 51    GEISPSNLVS   VQAQASGQIK   KLYVKLGQVQ   KKGDLIAEIN   STTQNTIDM  
 101   ESKSLETYQA   KLVSAQIALG   SAEKKYKRQA   ALWKDDATSK   EDLESAQDAL  
 151   AAAKANVAEL   KALIRQSKIS   INTAESDLGY   TRITATMDGT   VVAIPVEEGQ  
 201   TVNAAQSTPT   IVQLANLDM   LNMQIAEGD   ITKVKAGQDI   SFTILSEPDT  
 251   PIKAKLDSVD   PGLTMSGG   YNSSTDASN   AVYYYARFV   PNPDKLATG  
 301   MTTQNTVEID   GVKNVLLIPS   LTVKNRGGKA   FVRVLGADGK   AVEREIRTGM  
 351   KDSMNTVEKS   GLKEGDKVVI   SEITAAEQQE   SGERALGGPP   RR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

m290.seq (partial)  
 1    ..GTATCGGTCG   GCGCGCAGGC   ATCGGGGCAG   ATTAAGATAC   TTTATGTCAA  
 51    ACTCGGGCAA   CAGGTTAAAA   AGGGCGATT   GATTGCGGAA   ATCAATTCGA  
 101   CCTCGCAGAC   CAATACGCTC   AATACGGAAA   AATCCAAGTT   GGAAACGTAT  
 151   CAGGCGAAGC   TGGTGTCCGC   ACAGATTGCA   TTGGGCAGCG   CGGAGAAGAA  
 201   ATATAAGCGT   CAGGCGGCGT   TATGGAAGGA   AAACGCGACT   TCCAAAGAGG  
 251   ATTTGGAAAG   CGCGCAGGAT   GCGTTTGCCG   CCGCCAAAGC   CAATGTTGCC  
 301   GAGCTGAAGG   CTTTAATCAG   ACAGAGCAAA   ATTTCATCA   ATACCGCCGA  
 351   GTCGGAATTG   GGCTACACGC   GCATTACCGC   AACGATGGAC   GGCACGGTGG  
 401   TGGCGATTCT   CGTGAAGAG   GGGCAGACTG   TGAACCGGGC   GCAGTCTACG  
 451   CCGACGATTG   TCCAATTGGC   GAATCTGGAT   ATGATGTTGA   ACAAAATGCA  
 501   GATTGCCGAG   GCGGATATTA   CCAAGGTGAA   GGCGGGGCAG   GATATTTCTG  
 551   TTACGATTTT   GTCCGAACCG   GATACGCCGA   TTAAGGCGAA   GCTCGACAGC  
 601   GTCGACCCCG   GGCTGACCAC   GATGTCGTCG   GGCGGTACA   ACAGCAGTAC  
 651   GGATACGGCT   TCCAATGCGG   TCTACTATTA   TGCCCGTTGC   TTTGTGCCGA

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```

701 ATCCGGACGG CAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAATAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGCGTTTG TCGCGGTGT GGTGCGGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
1 ..VSVGAAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51 QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTMS GGYNSSTD TA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLI PSLTVKNRGG KAFVRVLGAD GKAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAEQ QESGERALGG PRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

m290.pep				10	20	30
				VSVGAAQASGQIKILYVKLGQ	QVKKGDLIAE	
g290	PQAAYTEAVRRGDISRTVSATGEISPSNLVSVGAAQASGQIKILYVKLGQ	QVKKGDLIAE				
	30	40	50	60	70	80
m290.pep		40	50	60	70	80
	INSTSQNTNLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD					
g290	INSTTQTNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATSKEDLESAQD					
	90	100	110	120	130	140
m290.pep		100	110	120	130	140
	AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST					
g290	ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPVEEGQTVNAAQST					
	150	160	170	180	190	200
m290.pep		160	170	180	190	200
	PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTMS					
g290	PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTMS					
	210	220	230	240	250	260
m290.pep		220	230	240	250	260
	GGYNSSTDASNAVYYARSFVFNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG					
g290	GGYNSSTDASNAVYYARSFVFNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG					
	270	280	290	300	310	320
m290.pep		280	290	300	310	320
	KAFVRVLGADGKAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG					
g290	KAFVRVLGADGKAEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG					
	330	340	350	360	370	380
m290.pep	PPRRX					
g290	PPRRX					
	390					



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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GGCGGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTACAGGCG GGCGACATCA GCCGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGGA AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAAATTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGA AGAGGGGCAG
601 AGTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGCGGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAAG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCGCTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTTGGGTGC AGACGGCAAG GCGCGGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAAY AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQV KKGDLIAEIN STSQTNTLNT
101 ESKSKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTMG
351 RDSMNTVEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```

                                     10      20      30
m290.pep                          VSUGAQAASGQIKILYVKLGQVKKGDLIAE
                                     |||
a290                               PQAAAYITETVRRGDISRTVSATGEISPSNLVSUGAQAASGQIKLYVKLGQVKKGDLIAE
                                     30      40      50      60      70      80

                                     40      50      60      70      80      90
m290.pep      INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
                                     |||
a290           INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD
                                     90     100     110     120     130     140

                                     100     110     120     130     140     150
m290.pep      AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
                                     |:
a290           ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
                                     150     160     170     180     190     200

                                     160     170     180     190     200     210
m290.pep      PTIVQLANLDMMLNKMQIAEGDITKVKGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
                                     |||
a290           PTIVQLANLDMMLNKMQIAEGDITKVKGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
                                     210     220     230     240     250     260

                                     220     230     240     250     260     270
```

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```

m290.pep      GGYNSSTD TASNAVYYYARSFV PNP D GK LATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               |||||||
a290          GGYNSSTD TASNAVYYYARSFV PNP D GK LATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKV VISEITAAEQQESGERALGG
               :|||||
a290          KAFVRVLGADGKAAEREIRTGMRDSMNTVEVKSGLKEGDKV VISEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttgaaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaag gcaaatcccg ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tcccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSVAASLKAR
51  LEKTYSAQDL KVLSVSETPV KGIYEVVVSG RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCO PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPDA
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGAAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTcagcggc AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCgtcggcga ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAA GAAGTGCCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTcag CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAAATCCC GGTcggcggc AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC

```

680

751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence &lt;SEQ ID 1220; ORF 292&gt;:

```

m292.pep
1  MKTKLIKILT PFTVLP LLAC GQTPVSNANA EPAVKAESAG KSVAA SLKAR
51  LEKTYSAQDL KVL SVSETPV KGIYEVV VSG RQIIYTD AEG GYMFV GELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQGFEN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILT PFTVLP LLAC GQTPVSNANA EPAVKAESAG KSVAA SLKAR LEKTYSAQDL					
g292	MKTKLIKILT PFTVLP LLAC GQTPVSNANA E SAVKAESAG KSVAA SLKAR LEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVL SVSETPV KGIYEVV VSG RQIIYTD AEGGYMFV GELIN IDTRKNL TEERAADLNKIDF					
g292	KVL SVSETPV KGIYEVV VSG RQIIYTD AEGGYMFV GELIN IDTRKNL TEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGFVGG SICDNPVAET TSLGEQGFENG TPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGFVGG SICDNPVAET TSLGEQGFENG TPTLRLPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPOX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCCGCT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAA AGCCATCAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATCCC GGTGCGCGC AGCATCTGCG ACAATCCGCT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCAACGGG GCGAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep     MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAVKAESAGKSVAAASLKARLEKTYSAQDL
a292          MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAVKAESAGKSVAAASLKARLEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep     KVLVSSETPVKGIYEVVVSQGRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
a292          KVLVSSETPVKGIYEVVVSQGRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep     ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
a292          ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep     ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
a292          ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep     RSQSGYSPMPQLEEIIRKNQX
a292          RSQSGYSPMPQLEEIIRKNQX
              250     260
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtcgtgct
 51  gggttcgggt gtcagaacat catcgaaacc ctttcctgcg gcgttacgac
101  gatattcgcc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcgcc tgcggcggtt caagtcgaat cggcggacgc gtggcgtgaa
201  gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgagggcgt gcgggaagcg gtatgcggac atcggggggc atagtgtatc
351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgcgc
401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcgtg
451  ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgtcgc
501  cgagggcgcc cgcgaaagtg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccaggggaac tctagagtcg
601  actgcagcag catgccctc...
  
```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAVWSVRA VRTSSNRFP ALRRYSARFP TIFPKPAGTP
 51  WRRVRRFKSN RRRRGVKPLK KPYLARGAEC RCRRAWTALS HNIAERARES
101  PRRCGKRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPPFVG LLFARGTLES
201  TAAACP...
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

682

m294.seq  
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC  
 51 GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC  
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT  
 151 TGGCATCGGG TCGCGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA  
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC  
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG  
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGCGG ATAGTGATAC  
 351 AATCCGTATC CGAGTTTTCG GTTTGGAGCA TCGTATGAGT ATTTATGCCG  
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG  
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTGCGG  
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTACAGG  
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG  
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG  
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT  
 701 TCGCCATCGC CGTCGTCAA AATGGCGGTT CCACACTGAC GGTCCGTTGG  
 751 TCGAAATACA TACACGCCGT CGTCTTTACC CATATGCTGC TGATTGTCTT  
 801 TTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep  
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRYSAFQP TIFPKPADTP  
 51 WHRVRRFKSN RMRGGKPLK KPYRPRGGC RCRRWTALS HNIAERARES  
 101 PRRCGKRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV  
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPEVVG LFFASGIVMA  
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTGVW  
 251 SKYIHAVVET HMLLIVFLAK AMFYISW\*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFFAALRRYSAFRPTIFPKPAGTPWHRVRRFKSN					
m294	MRITCAPMSLLSAAVWSIRVVRTSSNRFFAALRRYSAFQPTIFPKPADTPWHRVRRFKSN					
	10	20	30	40	50	60
g294.pep	RRTRGVKPLKKPYLARGAECRCRRWTALSHNIAERARESRRRCGKRYADIGGSDTIRI					
m294	RRMRGGKPLKKPYRPRGGGRCRRWTALSHNIAERARESRRRCGKRYADIGGSDTIRI					
	70	80	90	100	110	120
g294.pep	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEVVLVSVLHTGRVSREARREVEKAMSYR					
m294	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVVLVSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
g294.pep	AVRVMPFAVGLLFARGTLESTAAACP					
m294	AVRVMPFVVGGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq  
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC  
 51 GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC  
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT  
 151 TGGCATCGGG TCGCGCGGTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA  
 201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC  
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG  
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC  
 351 AATCCGTATC CGAGTTTTCG GTTTGGAGTA CCGTATGAGT ATTTATGCCG  
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG  
 451 TTTTGTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTGCTG  
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTACAGG  
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG  
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG  
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

683

```

701 TCGCCATCGC CGTCGTCAA ATGGCGCGT CCACACTGAC CGTCGGCTGG
751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

```

a294.pep
1  MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAPFR TIFPKPAGTP
51  WRRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
251 SKYIHTVVFET HMLLIVFLAK AMFYISW*

```

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRYSAPFR	TIFPKPADTPWHRVRRFKSN			
a294	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRYSAPFR	TIFPKPAGTPWHRVRRFKSN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGG	CRCRRAWTALSHNIAERARE	SPRRCGKRYADIGGDS	TIRI		
a294	RRTRGGKPLKKTYRPRRAE	CRCRRARTALSHNIAERARE	SPRRYGKRYADIGGDS	TIRI		
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVH	LYCAIAFVGGVFEVLVLSV	LHTGRVSREARREVEKA	MSYR		
a294	RVFRLEYRMSIYAVAHIVH	LYCAIAFVGGVFEVLVLSV	LHTGRVSCEARREVEKA	MSYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMPFVVGLLFASGIVMA	ANRYLSILGEPFATSFGTML	TLKILLAFSVLAHFAIAVVK			
a294	AVRVMPFVVGLLFASGIVMA	ANRYLSILGEPFATSFGTML	TLKILLAFSVLAHFAIAVVK			
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVVF	THMLLIVFLAKAMFYISW				
a294	MARSTLTVGWSKYIHTVVF	THMLLIVFLAKAMFYISW				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

```

g295.seq
1  atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
51  gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg
101 cgctgtgctgc cgacacggc aaccggccgg cctccgatgc gtttttcaa
151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc
251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca
351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgccg gcattccctt
401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggcg
451 gtgttcgcgc aaaaactgcc gtacccacgt tttttgtca tacggaagat
501 agcggcattg cgcatcggga aacagaactt gcgcggttcc ccgtcccgtc
551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgcgcaa
601 ctgcggtatc aagggtggg cggcacgcgt ttctccgacc gaaacggcgt
651 gtatccaaac cgcccggtta acgggattcg gatgcggctt gccgaaacgc
701 tcgtccctat gcgcccggta tgccggggca cttccggagc gtttgtcaa
751 ataacgccgt atccatatcg gcgcaagcag ccacaataca tcataaagcc
801 attggaacat cttctattt cctgcaaaac aaatgccgtc cgaacgggtc
851 ggacggcatt tcggcaacgg aatcaaatat cgtag

```

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pap  
 1 MLGMRHDDGQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK  
 51 LPRQRFHVR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLR QTARQSRGCG  
 101 TDQAADFQIT VQRFRRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA  
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ  
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ  
 251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVQTAFRQR NQIS\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq  
 1 ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCATATT  
 51 GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAAGC  
 101 CGCGTGTGCG CGCACACGGC AACCGGCCCG CCTCCGATGC GTTTTCAAA  
 151 CTGCCCCGCC AGCGTTTCA TCTGTTCCGA CGGTATGATG TCGTATTGG  
 201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC  
 251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG  
 301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA  
 351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC  
 401 ATCAGGTTGG GCCAGATTTT GGTTCATC AAAATGCCGA ACATCGGCGC  
 451 GTGTTCCGCG AAAAACTGCC GTACCCACGT TTTTGTGCA TACGGAAGAT  
 501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTT CCGCCCCGTC  
 551 GGGGTCTATCT GCGTCATCAG CAGCGCGCGA TCGGGAAC GCCGCCGCAA  
 601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGCGT  
 651 GTATCCAAAC CGCGCCGTA ACGGGATTTC GATACGGCTT GCCGAAACGC  
 701 TCGTCCCGAT CGGCCCGATA TGCCGGGCGA CTCCGGAGC GTTGTCCAA  
 751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGCC  
 801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC TGAACGGTTC  
 851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pap  
 1 MLGMRHDDQ QRIAAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK  
 51 LPRQRFHLFR RYDVVFGLAA HLHGCRAQFR QPRRIRLCLR QTARQSRGGR  
 101 TDQAADFQIT VQRFRRQPRI RQKQRHTRAP AFPHQVGPDF GFHQNAEHRA  
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRGHLRHQ QRRIGKTPPQ  
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ  
 251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTVQTAFRQR NQIS\*

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pap	MLGMRHDDQRIAAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPRQRFHLFR					
g295	MLGMRHDDGQGIQIAAILLPRRQOFFRLVFAPINARAAAHGNRPASDAFFKLPRQRFHVR					
	10	20	30	40	50	60
m295.pap	RYDVVFGLAAHLHGCRAQFRQPRRIRLCLRQTARQSRGGRTDQAADFQITVQRFRRQPRI					
g295	RHQVVFGLAAHLHGCRAQFRQPRRIRLRLRQTARQSRGGCTDQAADFQITVQRFRRQPRI					
	70	80	90	100	110	120
m295.pap	RQKQRHTRAPAFPHQVGPDFGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
g295	RQKQRHTRSPAFHLHQIGPDFGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
	130	140	150	160	170	180
m295.pap	PPRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI					
g295	PSRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRMRLAETLVPMRPV					
	190	200	210	220	230	240
m295.pap	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX					
g295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVRTVQTAFRQRNQIS					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTC TCTGTTCCGA CGGCATCAGG TCGTATTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTGAGCGAAG CGGCGGCGAG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCTTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTACC GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAC GCTGCCGCAA
601 CTCGCGTATC AAAGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA .ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCGCAT GCGCCCGATA TGCAGGGGCA CTTCCGAGC GTTGTGTC
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATGGAAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQQFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRHFLFR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLC QTARQSSGGR
101 TDQAADFQIT V*FFRQPRI RQQRHTRAP AFLHQIGPDF GFHQAETHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLQP
201 LAYQLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	QRIAAILLPR	RQQFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRHFLFR
a295	MLGMARHDDQ	QRIAAILLPR	RQQFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRHFLFR
	10	20	30	40	50	60
	70	80	90	100	110	120
m295.pep	RYDVVFGLAA	HLHGCRAQFR	QPRRIRLRLC	QTARQSSGGR	TDQAADFQIT	VQRRFFRQPRI
a295	RHQVVFGLAA	HLHGCRAQFR	QPRRIRLRLC	QTARQSSGGR	TDQAADFQIT	VXRRFFRQPRI
	70	80	90	100	110	120
	130	140	150	160	170	180
m295.pep	RQQRHTRAP	AFPHQVDFG	GFHQAETHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
a295	RQQRHTRAP	AFPHQVDFG	GFHQAETHRA	VFAQKLPYPR	FFVIRKIAAL	CIRKQNLRGF
	130	140	150	160	170	180
	190	200	210	220	230	240
m295.pep	PSRRGHLRHQ	QRRIGKTL	PQLAYQGLG	TRFSDNRGV	PNRAGNGIRI	LAETLVPMRPI
a295	PSRRGHLRHQ	QRRIGKTL	PQLAYQGLG	TRFSDNRGV	PNRAGNGIRI	LAETLVPMRPI
	190	200	210	220	230	240
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
a295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTAFRQR	NQISX
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```



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51  GCTTGCCGTT TCGATTATTC TGGTgtcgGC GGCATACATT GCTtcgacag
101 aggggaccga ggcggtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTTGGg ggggcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGgacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCCA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTCGC TTTGAAAAA AAAGCGGCA TATGGCGCGC GTCGGCTTCT
451 GATGCCGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGTCTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGGCGGCTT
801 CAACATCgag CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCCG AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TGC CGCGCGCG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSa REVQFTDED GERNLVALEK KGGIWRRSAS
151 DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDEKGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTTPVRA SADGVITFKG RKGGYGNAMV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGTGRST GPHLHYEARI NGQPVNPFVS ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCCGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA CGCGTCAGA CCGCAGCGCG TGAACAAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGCACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCCA
351 CGCGCGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCAGCGCA
401 ATCTGGTCGC TTTGAAAAG AAAGCGGCA TATGGCGCGC GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTCTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGCG
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 CCCGCACCCG AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TGC CGCGCGCG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RYALRALAV SIILVSAAYI ASTERTERV RQRVEQNLP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSa REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG  
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY  
 301 AAPQGTTPVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA  
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPFVSV ALPTPELTQA  
 401 DKAAFAAQKQ KADALLARLR GIPVTVSQSD \*

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQVEQNLPPLSWGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGERVRPQVEQKLPLSWGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDDEGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVVPV					
g297	REVQFFTDDEGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEVVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGTRHQAFY					
g297	EIRESLSGIFAGRFLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGTTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPFVSVALPTPELTQADKAAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPFVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCCGC	GGCATAACATT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGCAGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTTCAGACG	GATATTGGG	TGCAGGAGGC
201	GGTGACGCCA	GGCGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTTGG	TCGGCGGCGA
351	CGCGCGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCGC	TTTGGA AAAA	AAAGCGGCA	TATGGCGGCG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTTT	GCCGACGCTG	CGTTCGGTCG	TGGTCAAAAC
501	GTCGGCGCGC	GGTTCGCTGG	CGCGGCGGGA	AGTGCCCGTC	GAAATTCGCG

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGCGGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGC CGCGGCGG CGAGGTCATC GGT TTTGTCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGC GC CATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV RQVEQKLPP
51 LSWGGSGVQT AYWQEAQVQ GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGG REVQFFTTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPFL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDDEGRV LQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY
301 AAPQGTTPVRA SADGVITFKG RKG YGNVAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKH RKYALRALAVSIILVSAAYI ASTERTERV RQVEQKLPP LSWGGSGVQT					
a297	MAVFPLSAKH RKYALRALAVSIILVSAAYI ASTERTERV RQVEQKLPP LSWGGSGVQT					
	10	20	30	40	50	60
m297.pep	AYWQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGG					
a297	AYWQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGG					
	70	80	90	100	110	120
m297.pep	AYWQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGG					
a297	AYWQEAQVPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGG					
	70	80	90	100	110	120
m297.pep	REVQFFTTDEDGERNLVALEKKG IWRRSASEADMKVLPFLRSVVVKTSARGSLARAEVPV					
a297	REVQFFTTDEDGERNLVALEKKG IWRRSASEADMKVLPFLRSVVVKTSARGSLARAEVPV					
	130	140	150	160	170	180
m297.pep	REVQFFTTDEDGERNLVALEKKG IWRRSASEADMKVLPFLRSVVVKTSARGSLARAEVPV					
a297	REVQFFTTDEDGERNLVALEKKG IWRRSASEADMKVLPFLRSVVVKTSARGSLARAEVPV					
	130	140	150	160	170	180
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGTRHQAFY					
a297	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGTRHQAFY					
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGTRHQAFY					
a297	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQAAGDILAAEVVKGTRHQAFY					
	190	200	210	220	230	240
m297.pep	YRSDKEGGGGGNYDDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
a297	YRSDKEGGGGGNYDDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
a297	YRSDKEGGGGGNYDDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
m297.pep	AAPQGTTPVRASADGVITFKGRKG YGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
a297	AAPQGTTPVRASADGVITFKGRKG YGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRKG YGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
a297	AAPQGTTPVRASADGVITFKGRKG YGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
	310	320	330	340	350	360

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```

          370      380      390      400      410      420
m297.pep  GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a297      GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR
          370      380      390      400      410      420

          430
m297.pep  GIPVTVSQSDX
          ||||||||||
a297      GIPVTVSQSDX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

```

g298.seq
1  ATGAAAAACT TTCTTCCCT TTCGCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTT CCGCCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcgcgcac ggCTCAAGAC GGCCTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGAG ATTCGCTGAT GCAGGCGTTC GCGCCTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC CGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACT GAAAGGCAA ATCATCCTGA TTCCACCGC
801 GCAAACTAGT AGCGCGGGA AAGGccGCTA CACCGATTCC GTCACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGA AAAATA ATGGA AAAA TCGTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

```

g298.pep
1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKFTL SGETPPTAQD GGSADMPPPEA AASEAAPPAG
101 GTEWKQGTTEA AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNPD WDFPVGKRYL
201 KFASDEWAQE YLKRVDRILE AAHTRVQVW WLGIPLYMKKV KLDGQMRYLD
251 KLLSEHLKSK IILIPTAQL SGGKGRYTD S VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

```

m298.seq
1  ATGAAAAACT TTCTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTT CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CCGCGCGGAC GGCTCAAGAC GGCCTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCGGCG ACTCGCTGAT GCAGGCGGTT GCCCCTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC CGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATTT GAAAGGCAA ATCATCCTGA TTCCACCAC
801 GCACACCTGT AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGA AAAATA ATGGA AAAA TCGTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep  
 1 MKNFLSLFSS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR  
 51 SGAALQENAY ALSDGIKAPL SGETPPTAQD GGSADMPSEA AASEAVPQTG  
 101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS  
 151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL  
 201 KFASDEWAQE YLKRVDRIE AAHTRVQVW WLGIPIYMKKA KLDGQMRYLD  
 251 KLLSEHLKGI ILIPTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA  
 301 EGQKLLAAKI MEKIVFEPST QPSSTQP\*

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAPLSGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKAPLSGETPPTAQDGGSDMPSEAAASEAAPPAGGTGEWKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQQYGIESANLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPIYMKKA					
g298	LAVFLGPNDPWFDFPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPIYMKKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGIILIPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMRYLDKLLSEHLKGIILIPTAQLSGGKGRTDSDNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq  
 1 ATGAAAACT TTCTTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT  
 51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT  
 101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG  
 151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA  
 201 AGCCTTCCTG TCCGCGGAAA CGCCGCCGAC GGCTCAAGAC GCGGTTTCGG  
 251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAATGGC  
 301 GAAACAGAAT GGAAACAAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA  
 351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG  
 401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC  
 451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC  
 501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT  
 551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC  
 601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG  
 651 CATCCTTGAA GCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA  
 701 TCCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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751  AACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TTCCCACCGC
801  GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1   MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101 ETEWKQNTA AAVRTGDKVF FAGDSLQGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDR WDFPVGKRYL
201 KFASDEWAE YLKRVDRIE AAHTHYVQVW WLGI PYMKKA KLDGQMRYL
251 KLLSEYLGK IILIPHTAL SGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTA AAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDLSMQGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLQGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDEWDFPVGKLYLKFADEWAEYLYKRVDRILEAAHTRVQVWVWLGIPYMKKA					
a298	LAVFLGPNDEWDFPVGKRYLKFADEWAEYLYKRVDRILEAAHTHYVQVWVWLGIPYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLKLLSEHLKGIILIPHTALSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
a298	KLDGQMRYLKLLSEYLGKGIILIPHTALSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1   ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
51  GGCAGAAGCC CTGCCGCTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCGCGC CCTCGCCTTG GATGAAAAAA CTCCGATCCG TCGCACAAGG
201 CAGCGGCGAG GCCTTCCGCA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACGCC CTGCGCAAAC GCCTGCAAAA AACATGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA
401 ATACCGGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAC CCGCAGCGGC
451 GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTGACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCC TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACGCGCCCC GTCCCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGGCGGAA ATGCTTGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCGCGCGC CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
51 NAAASPWMKK LRSVAQSGE AFRILQIGDS HTAGDFFTD LKRLQKTWG
101 DGGIGWVYPA NVKGQRMMAV RHSGNWQSFT SRNNTGDFPL GGILAQTGSG
151 GGMTLTASDG KTGKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLAIQTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAADGVHF SAQGYRRAE MLADSLEELV RAAAIRQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

```

1 ATGAACCCCA AACACCTCAT CGCATTTCCT GCCCTATTCG CCGCCACGCA
51 GGCAGAAGCC CTACCTGTCT CCTCCGTGAG CCTCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGCGCAG ACCTTCCGTA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GCGAGCGCAT
351 GCGCGCGGTC CGGCACAACG GTAAGTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGTC GCGCGCATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTCG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
901 CTCATCATCG GCGCACCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCC
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC CATGGGCGGC
1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51 NASASPWMKK LQSVQSGE TFRILQIGDS HTAGDFFTD LKRLQKTWG
101 DGGIGWVYPA NVKGQRMMAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKNWLNQ GWAADGVHF SAKGYRRAE MLADSLEELV RSAAIRQ*

```

m299/g299 95.5% identity in 397 aa overlap

```

10 20 30 40 50 60
m299.pep MNPKEHIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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g299	MNPKHFIASFALFAATQAEALPVASVSPDTVTVSPSAPYTTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299. pep	LQSV AQSGSETFRILQIGDSHTAGDFFTD SLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
g299	LRSAVQSGSEAFRILQIGDSHTAGDFFTDALRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299. pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFSTRNNTGDFPLGGILAHTGSGGSMTLTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299. pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299. pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299. pep	LIIGAPESLKNLTGVCGRPVRLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNLTGVCGRPVLLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299. pep	GWAAKDGVHFSAGYRRAAEMLADSLLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAGYRRAAEMLADSLLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299. seq

```

1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GCGGCGCCGC CGGCACAACG GTAACCTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCCGCTC GCGGCGATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTA CTGGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCCGGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTGCGACA TGAAAACTG GCTCAACCAC GGATGGGCGG CCAAAGACGG
1101 CGTACACTTT TCCGCCAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

```



This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGQMAAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151  GSMTLTASDG IASKQVSLF AKPLLAETL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIADIAT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQQMQ RRIARQQQM FWSWQNAMGG
351  VCSMKNWLNH GWAADGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

	10	20	30	40	50	60
m299.pep	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
m299.pep	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
a299	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
	70	80	90	100	110	120
m299.pep	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
a299	LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKQORMAAV					
	70	80	90	100	110	120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
	130	140	150	160	170	180
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMILTASDGIASKQVSLFAKPLLAETL					
	130	140	150	160	170	180
m299.pep	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFNGDNIADIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFNGDNIADIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRVARQQQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRRIARQQQTMFWSWQNAMGGVCSMKNWLNH					
	310	320	330	340	350	360
m299.pep	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRVARQQQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRPVRRLTEVQQMQRRRIARQQQTMFWSWQNAMGGVCSMKNWLNH					
	310	320	330	340	350	360
m299.pep	GWAADGVHFSAGKYRRAEMLADSLEELVRSAAIRQX					
a299	GWAADGVHFSAGKYQSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTTACGCTT TTTATATTT TCATTGTGTT ATGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCGACTA TCCGTCCCGC ATCCGCGTCC
201  TGTGTTGGGC AAAGGACGTG CCGATGACGG TTTGATTAC GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
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695

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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACGCG TTTTATATGG
701 CAGCCAGTAC GTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCTTATCAA TCAGATTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGGCT CATCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTATT TTCTGTTGT
1001 TTGCGCTGCC GGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGTTTAA TTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGCGTA CGCGCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GGCAGCGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCTT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTTGT
1551 TTTGGGCTCG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVF TG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQI IHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIYPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFI LICA FI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIITPMN SYFGLIMATV IKYKGDAGVG TLISMMLPYS
501 AFFLIWIAL FCIWVFLGL PVGPGTPTFY PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATT TCAATGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCGC ATCCGCGCCC
201 TGTGTTGTCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACCGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGT ACTGAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCAGC CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGA GCATCGTCCC TGCCGACGGT
901 ATTTTGGCTC ATCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTAAAT
951 ATCGATTGTT GTTTTATT TCTGTTGTT TGCAGTGCY GGCmTTGTTT
1001 ATGGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

```

m302.ppt

m302/q302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAVGAYFGL					
	: :					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAAGRADDDLIIYVSVLLNADGPIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	: :					
g302	SVPDPRPVGAAGRADDLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGGLISALMRLLLTKSPRKLTTFMVVFITGILSNTASELGYVVLIPLSAII FHS LGRHPL					
g302	EKSGGLISALMRLLLTKSPRKLTTFMVVFITGILSNTASELGYVVLIPLSAII FHS LGRHPL					
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLIGITQQAAQIIHPDYVVGPEANWFMAASTFVI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPYQS DLSQE EKD I R H S N E I T P L E Y K G L I W A G V V F V A L S A L L A W					
g302	ALIGYFVTEKIVEPQLGPYQS DLSQE EKD I R H S N E I T P L E Y K G L I W A G V V F V A L S A L L A W					
	250	260	270	280	290	300
	300	310	320	330	340	350

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGFILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKGAGVGTLLISMMLPYSAFFLIWIALFCIWWFVLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      IKYKKGAGVGTLLISMMLPYSAFFLIWIALFCIWWFVLGLPVGPGPTPTFFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATATTTT TCATGTGTGT ATGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGAATA TCCGTCCCGC ATCCGCGCCC
201 TGTGGTGGCG AAAGGACGTG CCGATGACGG TTTGATTCAC GTTGTACAGC
251 TGCTCGATGC TGACGGTTTG ATCAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCGGTT GGAACGGGTG TTGTTTCTT TATGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGCTCTGG
551 TTCCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAAGTGG TTTTATATGG
701 TAGCCAGTAC GTTGTGATTG GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAAATTTGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGGCT CATCCTGAAA CAGGATTGGT
951 TTCCGGTTTC CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTATAATT
1151 TGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTTA TTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTGCTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTGTT
1551 TTTGGGCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDQTD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHNSEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIIVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPM SYFGLIMATV IKYKDGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

## m302/a302 96.1% identity in 533 aa overlap

```

-- 100 --
m302.pep      10      20      30      40      50      60
MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAVGAYFGL
|||||
a302          10      20      30      40      50      60
MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAAGAYFGL

m302.pep      70      80      90     100     110     120
SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLLGVGIA
|||||
a302          70      80      90     100     110     120
SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILHTVKNFTGFAPLGTVLVSLLGVGIA

m302.pep     130     140     150     160     170     180
EKSGLISALMRLLLTKSPRKLTFMVVFTGILSNTASELG YVVLIPLSAI IFHSLGRHPL
|||||
a302         130     140     150     160     170     180
EKSGLISALMRLLLTKSPRKLTFMVVFTGILSNTASELG YVVLIPLSAI IFHSLGRHPL

m302.pep     190     200     210           220     230
AGLAAAFAGVSGGYSANLFLSTIDPLACITHQAA-----VVGPEANWFFMVASTFVI
|||||
a302         190     200     210     220     230     240
AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAQIIHPDYVVGPEANWFFMVASTFVI

m302.pep     240     250     260     270     280     290
ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW
|||||
a302         240     250     260     270     280     290     300
ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW

m302.pep     300     310     320     330     340     350
SIVPADGILRHPETGLVSGSPFLKSIIVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
|||||
a302         300     310     320     330     340     350     360
SIVPADGILRHPETGLVSGSPFLKSIIVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE

m302.pep     360     370     380     390     400     410
SMSTLXLXIXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
|||||
a302         360     370     380     390     400     410     420
SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI

m302.pep     420     430     440     450     460     470
NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
|||||
a302         420     430     440     450     460     470     480
NLMIGSASAQWAVTAPIFVPMMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV

m302.pep     480     490     500     510     520
IKYKDGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
|||||
a302         480     490     500     510     520     530
IKYKDGAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq  
 1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG  
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG  
 101 GCAATCTGAT TGGTTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC  
 151 CAGCTCGGTG CCGTTTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG  
 201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC  
 251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT  
 301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT  
 351 GCTGTTTTTG GCGGTTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC  
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC  
 451 TTGATGATCG GTGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG  
 501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA  
 551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TTCCGATGAT GGTTCGAGCA  
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT  
 651 CGGTTTGATT TTGATAGGCT TTATGCTGCG TTTTGTTCG GGTTCGTTAG  
 701 CCGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT  
 751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGTTGTC  
 801 GGGCTGGATA AGTTGGGAAT GA

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep  
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI  
 51 QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF  
 101 DKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA  
 151 LMIGVAQVFA LVPGTSRSGS TVMGMLWGI ERKTATEFSF FLAVPMVAA  
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF  
 251 AYYRIVFGIV IILWLSGWI SWE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)  
 1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG  
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG  
 101 GCAATCTGAT TGGTTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC  
 151 CAGCTCGGTG CAGTTTTTGGC GGTAGTGTTT GAATACCGGC AACGTTTCAG  
 201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC  
 251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT  
 301 GGCawACAAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT  
 351 GCTGGTtyTG GrcGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC  
 401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC  
 451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG  
 501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA  
 551 CTGCGACAGA ATTCTCGTTT TTCTTGCTG TGCCGATGAT GGTTCGCCCA  
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT  
 651 CGGTTTGATT CTGATAGGCT TTATGCTGCT CTTTGTTCG GGTTCGTTAG  
 701 CGGTAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)  
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI  
 51 QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLAI AF IPAAVMGLLF  
 101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA  
 151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMVAA  
 201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

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	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
	:					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGMLWGI					
	:					
m305	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
	:					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTC  TGATTGTCCT  GAAAGCCCTG  ATGATGGGCT  TGGTAGAAGG
51  TTTTACCGAA  TTTTACCGA  TTCCAGCAC  CGGACATTG  ATTGTGTTG
101 GCAATCTGAT  TGATTTTAC  AGCAATCACA  AGGTTTTGA  AATTACCATC
151 CAGCTCGGTG  CGGTTTGGC  GGAGTGTGTT  GAATACCGGC  AGCGTTTCAG
201 CAATGTGTTG  CATGGCGTGG  GAAAAGACCG  GAAAGCCAAC  CGTTTCGTCC
251 TTAATCTTGC  CATGCTTTT  ATACCTGCCG  CCGTGATGGG  GCTGTGTTT
301 GGCAACAAA  TCAAAGAGTA  TCTGTTTAA  CCCTTGAGTG  TTGCAGTCAT
351 GCTGTTTTG  GCGGTTTTT  TTATTTGTG  GGTGGAGAAA  CGCCAAAGCC
401 GAGCAGAGCC  TAAATTTGTC  GATGTTGATG  CATTGCGTCC  GATTGATGCG
451 TTGATGATCG  GCGTTGCCA  AGTGTGCA  CTGGTCCAG  GTACGTCCC
501 TTCGGCAGT  ACGATTATGG  GCGGGATGCT  TTGGGGAATC  GAGCGGAAA
551 CGGCAACGGA  GTTTTCATT  TTCTTGCCG  TTCCGATGAT  GGTTCAGCA
601 ACGGCTTATG  ATGCTCTGAA  GCATTACCG  TTTTTCACCC  TGCATGATGT
651 CGGTTTGATT  TTGATTGGCT  TTGTTGCTG  CTTTGTTC  GGCTTGCTG
701 CCGTCAAAGC  GTTGCTGAGG  TTGTTTCCA  AGAAAATTA  TATTCCTTT
751 GCCTATTACC  GCATTGTTT  TGGTATTGCC  ATCATTATAT  TGTGGCTGTC
801 AGGCTGGATA  AGTTGGGAAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL  MMGLVEGFTE  FLPISSSTGHL  IVFGNLIDFH  SNHKVFEITI
51  QLGAVLAVVF  EYRQRFNSVL  HGVGKDRKAN  REVLNLAI  IPAAVMGLLF
101 GKQIKEYLFN  PLSVAVMLVL  GGFFILWVEK  RQSRAPKIV  DVDALRPIDA
151 LMIGVAQVFA  LVPGTSRSGS  TIMGMLWGI  ERKTATEFSF  FLAVPMMVAA
201 TAYDVLKHYR  FFTLHDVGLI  LIGFVAAFVS  GLVAVKALLR  FVSKKNYIPF
251 AYYRIVFGIA  IILWLSGWI  SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	:					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	:					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
a305	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAAGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GCACAGGCAG  TGCAGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAAG  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGawCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAwGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCCGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAAGAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```



702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG  
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA  
 701 GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG  
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)

1 ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPNQXX  
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP  
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA  
 151 SKEEKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR  
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP  
 251 MR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

	10	20	30	40
m306.pep	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPKX			
g306	MFMNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKPK			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
g306	NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRIICKWARMPTNPGARKGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPRWSVIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq

1 ATGTTTATGA ACAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT  
 51 CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTATC  
 101 TGAACCAAGAG CGGTCAAAT GCGTTCAAA TCCCGGTTCC GTCGAAGCAG  
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT  
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA  
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT  
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGG  
 351 AAAGTCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACG GAAGAGCGTG  
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA  
 451 AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAGA  
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC  
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

a306.pcp

```

1 MFMNKFSSQS KGLSGFFFL ILATVIIAGI LFYLNQSSQN AFKIPVPSKQ
51 PAETEILPKP NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADQKPV
101 AAKADEVEEK ADEPEREKSD QAOVRKALKI EEREQTVEQK AQKQDAETVW
151 KQAVKPSKET EKKASKEKK AEKEKVPKPT TPEQILNSGS IEKARSAAK
201 EVQKMTKPTR RKQRIICKWA RMPTAGARKS SVPNQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

```

                                10      20      30      40
m306.pep      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETILKPKX
a306           MFMNKFSQSGKLSGFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETILKPK
                10      20      30      40      50      60

                50      60      70      80      90      100
m306.pep      NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREFPD
a306           NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEXAADKQPVADKADEVEEKADEPEREKSD
                70      80      90      100      110      120

                110     120     130     140     150     160
m306.pep      GQAVRKKALTEEREQTVREKAQKKDAETVKKQAVKPSKETTEKKASKEEKKAKEKVAPKP
a306           GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETTEKKASKEEKKAKEKVAPKP
                130     140     150     160     170     180

                170     180     190     200     210     220
m306.pep      TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
a306           TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                190     200     210     220     230     240

                230     240     250
m306.pep      LPRWSVIRRDIKRFTGCKAAICLPMRX
a306           LPRWSVIRRDIKRFTGCKAAICLPMRX
                250     260

```

g307.seq

1	atgaaaaacct	tcttcaaaac	cctttcgacc	gcgtcactcg	cgctcatcct
51	cgcagcctgc	ggcgggtcaaa	aagacagcgc	gccgcgagcc	tctgccgccg
101	ccccttctgc	cgataacggc	ggcgcgaaaa	aagaaatcgt	cttcggcgacg
151	accgtggggc	acttcggcga	tatggtcaaa	gaacaaatcc	aagccgagct
201	ggagaaaaaaa	ggctacacgc	tcaaattggt	cgaatttacc	gactatgtgc
251	gccccgaatct	ggcattggcg	gagggcgagt	tggacatcaa	cgttttccaa
301	cacaaacccct	atcttgacga	tttcaaaaaa	gaacacaacc	tggacatcac
351	cgaagccttc	caagtcgccga	cgcgcctttt	gggactgtat	ccggggcaaac
401	tgaaatcgct	ggaagaagtc	aaagacggca	gcaccgtgat	cgcgcccaac
451	gaccctgccca	acttcgcacg	cgcttgggtg	atgtcgtaac	aactggggtg
501	gatcaaaactc	aaagacggca	tcaatccgct	gaccgcatcc	aaagccgaca
551	tcgcggaaaa	cctgaaaaaac	atcaaaatcg	tcgagcttga	agcccgcaaa
601	ctgcgcgcga	gcccggccga	cgctggatttt	gccgtcgta	acgggaacta
651	gcgccataagc	agcggcatga	agtcgcacga	agccctgttc	caagaqccga

g307.pcp

m307.seq (partial)

m307.pep (partial)

m307/g307

a307.seq

a307.pcp

1 MKTFFKTLA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVEGTT

705

```

51  VGDFGDMVKE QIQPELEKKG YTVKLVEFTD YVRPNLALAE GEXDINVFOH
101 KPYLDDFKKE HNLDITEVFQ VPTAPLGLYP GKLSLEEVK DGSTVSAPND
151 PSNFARVLVM LDELGWIKLK XGINPLTASK ADIAENLKN I KIVELEAAQL
201 PRSRADVDFX VVNGXYAISS GMKLTEALFQ EPSFAYVNWS AVKTADKDSQ
251 WLKDVTEAYN SDAFKAYAHK RFEGYKSPAA WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
      220      230      240      250      260      270

                                39
m307.pep      AWNEGAAXK
      |||||
a307      AWNEGAAXK
      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTGTGA
51  TCCGTGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAGT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGTG TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGGA
501 AACGCGCGTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAGCGCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1278; ORF 308.ng&gt;:

```

g308.pep
1  MLNRVIFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RRMVRRLLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFQDNLLTRA
151 ADVVLKERRR LVLMVRETPL NLAHLNMRK VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTGTGA
51  TCCGTGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGGTGAAGG CTTTGGAAGT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGcT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGC CGGA
501 AACGCGCGTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GwAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGcTt TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CCGCGGAATG GCArgGAATG gcG...

```

This corresponds to the amino acid sequence &lt;SEQ ID 1280; ORF 308&gt;:

m308.pep (partial)

706

```

1  MLNRFVYRIL  GVADNLYPRL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMR  XTEGGGVFP  PVPAMYRKQP
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng)

from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRFVYRILGVADNLYPRLSDFCFFTI	IAGLPLQAVLWERRMMVRRLLII	GISGASGFQY			
g308	MLNRFVYRILGVADNLYPCLSDFCFFTI	IAGLPLQAVLWERRMMVRRLLII	GISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADFVHPIGNIGACIASGTF				
g308	GVKALELLRAQDVETHLVVSKGAEMARASE	TDYTKDEVYALADFVHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRA	ADVVLKERRRLVLMVRETPLNLAHLNMR				
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRA	ADVVLKERRRLVLMVRETPLNLAHLNMR				
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEGGGVFPVPVPAMYRKQP	TADDIVAHSAHALSLFGIDTPDSAEOQGM				
g308	VTEGGGVFPVPVPAMYRKQP	TADDIVAHSAHTLSLFGIDTPDLAEOQMAD				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTGTCCTG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTGCTGCAC  GGCTTCGGCG  ACAACCTCTT  TCGCGTGCCT
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTCTCTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMR  VTEGGGVFP  PVPAMYRKQP
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVYRILGVADNLYPRLSDFCFFTTI	AGLPLQAVLWERRMMVRRLLI	IGISGASGFQY			
a308	MLNRIFYRILGVADNLYPYLSDFCFFTTI	AGLPLQAVLWERRMMVRRLLI	IGISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADFVHPIGNIGACIASGTF				
a308	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALADKVHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGF	GDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR				
a308	KTDGMLVAPCSMRTLASVVGFGD	NLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR				
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRK	PQTADDIVAHSLVHALSLFGIDTPD	SAEWQGM			
a308	VTEMGGVVFPVPAMYRK	PQTADDIVAHSLVHALSLFGIDTPD	SAEWQGMAD			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCCTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCT AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCT TGTGCGGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCT CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVYRIL GVADNLYPCL SDFCFFTTIA GLPLQAVLWE RRMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPK
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCCTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCT AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCTCTGT TCGATGCGGA
401 CGCTTGCCCT TGTGCGGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCT CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTGCTGT
651 CGGAATCGAT ACGCCGGATT CCGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVYRIL GVADNLYPRL SDFCFFTTIA GLPLQAVLWE RRMVRRLLI

```

708

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA  
 101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA  
 151 ADVVLKERRR LVLMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKQ  
 201 TADDIVAHSV AHALSFGID TPDSAEWQGM AD\*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308-1	MLNRFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
m308-1.pep	VTEMGGVVFPVPAMYRKQQTADDIVAHSAHALSFGIDTPDSAEWQGMADX					
g308-1	VTEMGGVVFPVPAMYRKQQTADDIVAHSLFGLIDTPDLAEWQGMADX					
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRKQQTADDIVAHSAHALSFGIDTPDSAEWQGMADX					
g308-1	VTEMGGVVFPVPAMYRKQQTADDIVAHSLFGLIDTPDLAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA  
 51 TCCGTATTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTTCGCCGT  
 101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC  
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGGANCT  
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGTATCG AAAGGTGCGG  
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC  
 301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG  
 351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCCCTCTGT TCGATGCGGA  
 401 CGCTTGCCCT GGTGCTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG  
 451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCAGCA  
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA  
 551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAACCGCAG  
 601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT  
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGAATG GCGGATTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1288; ORF 308-1.a&gt;:

a308-1.pep

1 MLNRFYRIL GVADNLYPYL SDFCFFTTII GLPLQAVLWE RRMVRRLLI  
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA  
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA  
 151 ADVVLKERRR LVLMVRETPL NLAHLDNMXR VTEMGGVVFP PVPAMYRKQ  
 201 TADDIVAHSV AHALSFGID TPDSAEWQGM AD\*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRFYRILGVADNLYPYLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
m308-1	MLNRFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
a308-1	KTDGMLVAPCSMRTLASVHGFNDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
m308-1	KTDGMLVAPCSMRTLASVHGFNDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVHGFNDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
m308-1	KTDGMLVAPCSMRTLASVHGFNDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
	130	140	150	160	170	180

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPNLNLAHLNLMKR
              130      140      150      160      170      180

a308-1      190      200      210      220      230
VTEMGGVFPVPVPMYRKPTADDIVAHSAHALSLFGIDTPDSA EWQGMADX
|||||
m308-1      VTEMGGVFPVPVPMYRKPTADDIVAHSAHALSLFGIDTPDSA EWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1  atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgccg gcgcgctttg ggggtgtttg
101 gtttgaaaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaacacgtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggatcggca tcaatttcgt gctgcccag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctggt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttga aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgccg taccgcgatt
701 tgtcgccctt gggcgcgga tggcgggaaa aggcggatgg aaatgtccgc
751 atcgctcggt gcgcgctgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgca caggctttgg
851 gcatacgcaa ccactaccgc caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtta cggttgacgc gctcaccgat gacggacatt
1001 atctcgcgcg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg caccggcgtt tgaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcgcgcgcg cgaaagtcgc
1251 cgaagccctg ccgcctgcat ttttgccgga aaataccgtg gcgctggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1  MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGILITV RAGGKTAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET LLAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGT VKG VDGRGVLHLE TAEGEQTVVS GEISLRPDNR SVSVKRPDS
201 ERFLLEGGN SRLKWAVVEN GTFATVGSAP YRDLSP LGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNLGSRFRFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNVASGMM DAVCGS IMM HGRLEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1  ATGTTCAAGT TTGCTGGGT GTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCTT GTTGC GG CAG TGGCGTGT CG GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCAATTAAAG TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CCGCGGGATT

```



710

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCGCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAATGTCC
551 GCATCGTCGG TTGCGCTGTG TCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCGGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAAGT GCGGCACGGC GGTAAACGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrGGAACCA TCATGCCCGG TTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTCGCGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGGCGCGCG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAATA CCGTGCCTGT
1101 GCGGACAAC CTCGTCATTT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
51 KLGGILIETV RTGGKTAVAV GIGINFVLPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WVENGTFATV GSAPYRDLSP LGAWEAKAD GNVRIVCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTTGNAV ASGMDAVCG SVMMHGRLK EKTGAGKPDV VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

          10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILIETV
          10      20      30      40      50      60

          70      80      90      100     110
m311.pep RTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADAVALLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADAVALLETLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXXXXXXX
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDRGVLHLETAEGEQTIVVS
          130     140     150     160     170     180

          120     130     140     150     160     170
m311.pep XEISLRSDXRPVSVXKRRDSEFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      GEISLRPDNRSVSPKRPDSERFLLLEGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE
          190     200     210     220     230     240

          180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYFPFTTTGNAVASGMDAVCGSVMMHGRLEKKTGAGKPDVVIITGGGAAKVAEA					
g311	PAGKRYFPFTTTGNAVASGMDAVCGSIMMHGRLEKKTGAGKPDVVIITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1  ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATCTGAT TGAAACGGTC AGGACGGGCG GCAAACCGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCTG GCTGCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCGGATGCGG CCGTGTGCT GGAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA TATGCGCGGG ACGGATTTGC GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGCGCTTCT
501 GCACTTGGAA ACGGCAGAGG GCAAACAGAC GGTCTGCAGC GGCGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAGCG GCGGGATTCTG
601 GAACGTTTTC TGCTGTTGGA CCGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAGAA GGCACGTTTC CAACCGTCGG TAGCGCGCCG TACCGGATT
701 TGTCGCTTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CCGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGCTGT
951 CAGTTGCGGC ACGGCGGTAA CCGTTGACGC GCTCACCAGT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCGGA CCGCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGCGGTT TGAAAGAAAA AACCAGGGCGG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGGCGCGCG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGTCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1  MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIETV RTGGKTVAVV GIGINEVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLHE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLLDGGN SRLKWAVEN GTFATVGSAP YRDLSPLGAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYFPFTT TGNASGMM DAVCGSVMM HGRLEKKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLXXXXXXXX-----					
a311	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLLETLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV DGQGV LHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSVXKRRDSE RFLLLDGGNSRLK WAWVENGTFATVGSAPYRDL SPLGAE					
a311	GEISLRSDDRPVSVPKRRDSE RFLLLDGGNSRLK WAWVENGTFATVGSAPYRDL SPLGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFIRNHYRHPEEHGSDR					
a311	WAEKVDGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTD DGHYLG GTIMP GFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSRNACVVVSCGTAVTVDALTD DGHYLG GTIMP GFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYFPFPTTGNASGMMDAVCGSVMMHGR LKEKTGAGKPV DVIITGGGA AKVAEA					
a311	HAGKRYFPFPTTGNASGMMDAVCGSVMMHGR LKEKTGAGKPV DVIITGGGA AKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLN MIAAEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLN LIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGCGG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAAGGTCG GGTTCAGCAG
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTCACT TCGGCTGGG CGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTTGCGTGCC GCGCGGCTTT
501 GGGGTGTTTG GGTGTTGAAA CGCAAATCAA GTGGCCAAAC GATTGTTGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAACCGG TTGCGGTGGT CGGTATCGGC ATCAATTTCTG TGCTGCCCAA
651 GGAAGTGGAA AACGCGCTT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GCGGGGCGAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGCAGAA
751 CTGGGCGCGG TGTTGGAACA ATATGCGGAA GAAGGGTTCTG CGCCATTTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGCAGCG CGAAACCGTG TCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTGGA AACGGCAGaa ggCGAACAGA cggtcGtcag
951 cggcGaaATC AGcCTGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC Ggaacgtttt tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGcggt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcGCC
1101 gtaCCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAAG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCGCG
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCCT TCCCGACCAC AACGGGCAAC GCCGTGCGAA CGCGCATGAT
1551 GGACGCGGTT TCGGCGTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCGTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTVLKPSHWR VLAELADGLP OHVSQLAREA DMKPQQLNGF WQOMPABIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTLKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLEMS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETOIKWPN DLVVGRDKLG GILIEVTRAG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVDDG
301 RGVHLETAEE GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIWG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHE EHGSDRWFA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDG YLGGTIMGF HLMKESLAVR TANLNRPAKG
501 RYFPFTTTGN AVASGMMDAV CGSIMMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAELPFA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGCGCGA CATACGCGGG
151 CTGTTGCCGC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTTGACC GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGTC GGCGCGCCTT
501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTTGGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTGGA AACGGCAGAG GGCAAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGCGGATTC GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGGAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCCTGTGT CCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCGCG
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTGCGCA CGCGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGCG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCGTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1298; ORF 311-1&gt;:

m311-1.pep

```
1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDAPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILIETVRTG
201 GKTVAVVVIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLEVE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEGTVKGVDS
301 QGVHLHLETAE GKQTVVSGEI SLRSDDRVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSSAQAL GIRNHYRHFE EHGS DRWFNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*
```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
g311-1	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
g311-1	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
g311-1	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
g311-1	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
g311-1	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
g311-1	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
g311-1	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
g311-1	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
g311-1	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMI AEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCCGC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTC
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCA GTTGGCTGGG TGTGTTGACC GCCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGCC GCGCGCCTT
501 GTCGCGTTTG GGTGTTGAAA CGCAAAATCA GTGGCCAAAC GATTGTTGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTTC TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGAAT TGCCGATGCC GCCGTGTTGC TGGAAACGGT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTTC CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGACGGA
901 CAAGGCGTTC TGCACTTGA AACGGCAGAG GGCAACAGA CGGTCGTAG
951 GCGCGAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCGGAAGC
1001 GCGCGGATTG GGAACGTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGAATA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TCGGCGGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCAG
1401 TGACCGACAT TATCTCGGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAGATTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGGCTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTVLKPSHWR VLAELADGLP QHVSQALMA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGER SFGTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDFRPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILIVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEETVKGVDG
301 QGVHLHETAE GKQTVVSGEI SLRSDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAFYRD LSPLGAWEAE KVDGNVRIVG CAVCGEFKKA
401 QVQELARKI EWLPSSAQAL GIRNHYRHE EHGSDRWANA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

a311-1.pep      10      20      30      40      50      60
MTVLKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
|||||
m311-1          10      20      30      40      50      60
MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR

a311-1.pep      70      80      90      100     110     120
LVRPLAVFDAEGLRELGERSGFGTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
|||||
m311-1          70      80      90      100     110     120
LVRPLAVFDAEGLRELGERSGFGTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK

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a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGEC	LMFSFGWVDRPQYELG	SLSPVAACRRALSRL	GLKTQIKWPN		
m311-1	GRGRQGRKWSHRLGEC	LMFSFGWVDRPQYELG	SLSPVAACRRALSRL	GLDQIKWPN		
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIE	TVRTGGKTVAVVGIG	INFLPKVEENAASVQ	SFQTASRRGNADA		
m311-1	DLVVGRDKLGGILIE	TVRTGGKTVAVVGIG	INFLPKVEENAASVQ	SFQTASRRGNADA		
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVL	LQYARDGFAPFVAEY	QAANRDHGKAVLLLR	DGETVFEGTVKGVDG		
m311-1	AVLLETLLVELDAVL	LQYARDGFAPFVAEY	QAANRDHGKAVLLLR	DGETVFEGTVKGVDG		
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQT	VVSGEISLRSDRPVS	VPKRRDSEFLLLDGG	NSRLKWAWVENGTF		
m311-1	QGVHLHLETAEGKQT	VVSGEISLRSDRPVS	VPKRRDSEFLLLDGG	NSRLKWAWVENGTF		
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSP	LGAEWAKEVDGNVRI	VGCAVCGEFKKAQVQ	EQLARKIEWLPSSAQAL		
m311-1	ATVGSAPYRDLSP	LGAEWAKEVDGNVRI	VGCAVCGEFKKAQVQ	EQLARKIEWLPSSAQAL		
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPPEHGS	DRWFNALGSRFRSRN	ACVVVSCGTAVTVDAL	TDGHHYLGGTIMP	GF	
m311-1	GIRNHYRHPPEHGS	DRWFNALGSRFRSRN	ACVVVSCGTAVTVDAL	TDGHHYLGGTIMP	GF	
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANL	NRHAGKRYPFPTTGN	AVASGMMDAVCGSV	MMHGRLEKKTGAGKP		
m311-1	HLMKESLAVRTANL	NRHAGKRYPFPTTGN	AVASGMMDAVCGSV	MMHGRLEKKTGAGKP		
a311-1.pep	550	560	570	580	590	
	VDVIITGGGA	AKVAEALPPAFLAENT	VRVADNLVIHGLLN	LIAEGGESEHTX		
m311-1	VDVIITGGGA	AKVAEALPPAFLAENT	VRVADNLVIYGLLN	MIAEGREYEHIX		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT ttgcacgact
101 gcacgagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTccgcCAA
201 ATACGCGGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTGCGCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTGCGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGCGG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGGTC TGCTCCGTTG GTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGCG AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

... This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

```

g312.pep
1  MSIQSGEILE TVKMOVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FCGAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCETH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGQLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

```

m312.seq
1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51  CCAGAAATTT GATGTCCGCA CCATTACCAT CGGCATTGAT TGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTGAACCC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCACAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTCGCcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCGCCA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAATAATTGT CGTGTCTGTC AACCGGTGG AAGACAACCC GTTTwTGGCG
601 GCGCGGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAT TACCCGCGTG
751 GCGGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCCTTGG
801 TATTCTCGAC TTGTGCGCGA CCCC GCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCGGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTGGGCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

```

m312.pep
1  MSIQSGEILE TVKMOVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51  TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVXSIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FCGAKIVVFC NAVEDNPFXA
201 GAFHGSGLAV INVGVSGPGV VKAALENS DA TLTTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCETHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIIVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLGYAPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

m312.pep	10	20	30	40	50	60
	MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTGVKDLVTT					
g312	10	20	30	40	50	60
	MSIQSGEILETVKMVADNRNFDVRTITIGIDLHDCISTDIDVLNQNIYNKITTGVKDLVAT					
m312.pep	70	80	90	100	110	120
	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
g312	70	80	90	100	110	120
	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
m312.pep	130	140	150	160	170	180
	QKGMSPSDEVLIRSIPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	130	140	150	160	170	180
	QKGMSPSDEVLIRSVPEAMKTTDIVCSSNIGSTRAGINMDAVKLAGETIKRTAEITPEG					
m312.pep	190	200	210	220	230	
	FGCAKIVVFCNAVEDNPFKAGAFHSGS--DAVINVGVS GPGVVKAALENS DATTLTEVAE					
g312	190	200	210	220	230	
	FGCAKIVVFCNAVEDNPFMAGAFHSGSEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
m312.pep	240	250	260	270	280	290
	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	240	250	260	270	280	290
	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTAVGDSVARILEEMGLSVCGTH					
m312.pep	300	310	320	330	340	350
	GTTAALALLNDVAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	300	310	320	330	340	350
	GTTAALALLNDVAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
m312.pep	360	370	380	390	400	410
	CSVGLDMIIVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVDGTVFEGGLLG					
g312	360	370	380	390	400	410
	CSVGLDMIIVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVDGDSVEFEGGLLG					
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
g312	420	430	440			
	YAPVMPAKEGSCEVFVNRGGRIAPVQSMKNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTTC	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAATC

a312.pep

```

1      MSIQSGEILE TVKMVADQNF DVRTITIGID LHCDCISTDID VLNQNIYNKI
51     TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101    LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151    IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVFVC NAVEDNPFMA
201    GAFSGSGEAD AVINVGVSVP GVKKAALENS DATTLTEVAE VVKKTAFKIT
251    RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSLVCGTH
301    GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351    LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401    IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRRG RIPAPVQSMK
451    N*

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	10	20	30	40	50	60
m312.pep	MSIQSGEILETVK	MVADQNFDV	RTITIGIDL	HDCISSDIN	VLNQNIYN	KITTVGKDLVTT
a312	MSIQSGEILETVK	MVADQNFDV	RTITIGIDL	HDCISTDID	VLNQNIYN	KITTVGKDLVAT
	10	20	30	40	50	60
m312.pep	70	80	90	100	110	120
	AKYLSAKYGVPIV	NQRISVTP	IAQIAAATH	ADSIVSVAQ	TLDKAAKA	IGVSFIGGFSALV
a312	AKYLSAKYGVPIV	NQRISVTP	IAQIAAATH	ADSIVSVAQ	TLDKAAKA	IGVSFIGGFSALV
	70	80	90	100	110	120
m312.pep	130	140	150	160	170	180
	QKGMSPSDEV	LIRSIPEAM	KTTDIVCX	SINIGSTR	AGINMDAV	KLAGETVKRTAEITPEG
a312	QKGMSPSDEV	LIRSIPEAM	KTTDIVC	SSINIGSTR	AGINMDAV	RLAGETIKRTAEITLEG
	130	140	150	160	170	180
m312.pep	190	200	210	220	230	
	FGCAKIVVFC	NAVEDNPF	XAGAFHGS	G--DAVIN	GVSGPGV	VVKAALENS
a312	FGCAKIVVFC	NAVEDNPF	MAGAFHGS	GGEADAV	INVGVS	GPVVKAALE
	190	200	210	220	230	240
m312.pep	240	250	260	270	280	290
	VVKKTAFK	ITRVGELI	GREASKML	NIPFGIL	LDLS--PT	PPVGDSVA
a312	VVKKTAFK	ITRVGELI	GREASKML	NIPFGIL	LDLSLAPT	PAVGDSVA
	240	250	260	270	280	290
m312.pep						
a312						

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	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GT	TAALALLND	AVKKG	MMAS	SAV	GGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV
a312	GT	TAALALLND	AVKKG	MMAS	SAV	GGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSV	GLDMIA	VP	GDT	PAHTIS	GGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG
a312	CSV	GLDMIA	VP	GDT	PAHTIS	GGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAP	VMFV	KEGS	CEV	FVNR	GGRIAPAPVQSMKNX
a312	YAP	VMFV	KEGS	CEV	FVNR	GGRIAPAPVQSMKNX
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 cgcgcaaaag tttggttgcc gttttgcttg cagcgctgct tcaagaaccg
151 ctcggtttat cgcacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taaggcgccg aaaggcggtg
251 caacggcatt gggcgctgct ctggcactct ctcccgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcattc ggcttcaaag tatcctccct
351 tgcgcgctg gtcgccacaa ccgcgcggcc ccttgccgca ctgtttttta
401 tgcgcacata ttcttggtat ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaagaaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKAALTL LGDAAGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATAGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATAAPLAA LFFMPHTSWI FATLAIALLV
151 LLRHKSNILN LIKGESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGCT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCGCAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTG GGCTTCAAGG TGCTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTGCGGCA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKAALTL LGDAAGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATAGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNIKV LEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

from *N. gonorrhoeae*:

	10	20	30	40	50	60
m313.pep	MDDPRTYGS	GNPGATNVL	RS	GKKKAAAL	TLLGDAAKGL	VAVLLARVLQ
g313	MDDPRTYGS	GNPGATNVL	RS	GKKKAAAL	TLLGDAAKGL	VAVLLARVLQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGH	MWPVFFG	FKGKG	GVATALG	VLLALSP	ATALVCALI
g313	VALAALVGH	MWPVFFG	FKGKG	GVATALG	VLLALSP	ATALVCALI
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVA	ASFFMPH	VS	WVWATVA	IA	ALLVLF
	:			:		:
g313	VATTAAPLA	AALFFMP	HTSWIF	FATLAI	AILVLL	LRHKS
	:			:		:
	130	140	150	160	170	

a313.seq

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

```

1  MDDPRTYGSQ NPGATNVLRG GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFGFGKGG KGVALALGVL LALSPTTALV
101 CALIWLWMAF GFKVSSLAAL TATIAAPLAA LFEMPHTSWI FATLAIAILV
151 LLRHKSNIIL LIKGKESKIG EKR*

```

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRS	GKKKAAALT	TL	LGDAAKGLVAVLLARVL	QEPLGLSDSAIAA	
a313	MDDPRTYGSNPGATNVLRS	GKKKAAALT	TL	LGDAAKGLVAVLLARVL	QEPLGLSDSAIAA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKG	GKVATALGVLLALSPATAL	VCALIWLVM	AFGFKVSSLAAL		
a313	VALAALVGHMWPVFFGFKG	GKVATALGVLLALSP	TALVCALIWLVM	AFGFKVSSLAAL		
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVVAASFFMPHVS	WWATVAIALLVLF	FRHKS	NI	VKLLEGRESKIGGSRX	
a313	TATIAAPLAALFFMPHTS	WIFATLAIAILVLLR	HKSNI	LNLIK	GKESKIGEKRX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
1  atgaaattac aacaattggc tgaagaaaaa atcggcggtc tgattgtgtt
51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101 cctttaccaa ggcggcaaca cagccggcgc cgggctgtaa gccttacaat
151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacia
201 ctgccactct caaatgattc gtccgttcgg tgcggaaacc gagcgttacg
251 gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
301 ggttccaaac gtaccggtcc tgatttggca cgtgtgggeg gccgctattc
351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgctg
401 agtccaatat gccggcattc ccgtggcttg cagcaataa agtcgatgtc
451 gatgaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501 cagtgatgag gaaattgcca aagcgctga ggctttggca aacaaatccg
551 agctggatgc ttagtcgcc tatctgaag gattgggtct ggctttgaaa
601 aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
1  MKLQQLAEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVAVV YLQGLGLALK
201 NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGGCAACA CAGCCGGCGC CGGGCTGAA GCCTTACAAT
151 CCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCGG TCGGAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCGG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGCAATC CCGTGGCTTG CAGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTGAAA
601 AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
1  MKLQQLAEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVAVV YLQGLGLALK
201 NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401
10      20      30      40      50      60
m401.pep  MKLQQLAEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
g401      MKLQQLAEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
```

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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GGC GGCAACA CAGCCGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACCC GAGCGTTACG
251 GTCATTACTC TGTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAE EK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401.pep  MKLQQLAE EKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
a401      MKLQQLAE EKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSDEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVPESNMPAFPPWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG  TGAACACTAA  Accgaatact  agtgtgatta  atatgctttc
51  tttccttacc  ggatTATTGA  GCTTGGGTat  agaagtCtTg  tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag  tccgtgcctc  aggCATTtTC  atttattcett
151 gcctGtttttc tgACCGgtat  cgccgtcggc  gCgTATTTTG  GCAAACGGAT
201 TTGCCGCAGC  CGCTTGTGTG  ATATTCcctT  TATCGGGCAG  TgcttcttgT
251 GGGCGGGTAT  TgccgaTttt  ttgatTTTGG  GTGCTGCGTG  GTTGTGACG
301 GGTTTTTTccg gtttcGTCCA  CCACGCCGGT  AtttTCATTA  CCCTgtctgc
351 CGtcGTCAGG  GGGTTGATTT  TCCCACTTGT  ACACCATgtg  GGTACGGATG
401 GCAACAAATC  CGGACGACAG  GTTCCAATG  TTTATTTGCG  CAACGTGACC
451 GGCAGTGCAT  TGGGTCCGGT  CCTATCGGC  TTTGTGATAC  TTGATttgtt
501 gTCCACCCAA  CAGATTtacc  tgetcatCTG  TTTGATTtCT  GCTGctgtcc
551 cTTTGTtTTg  tacaCTGtTC  CAAAAAGTC  TCCGACTGAA  TGCAGTGTcG
601 GTAGCAGTTT  CCCTAATGTT  CGGCATCCTC  ATGTTCTTAC  TGCCGGATTc
651 TGTCTTTCAA  AATATTGCTG  GCCGTCCGGA  TAGGTTGATT  GAAAACAAAC
701 ACGGCATTGT  TGCGGTTTAC  CATAGAGATG  GTGATAAGGT  TGTtTATGGG
751 GCGAATGTAT  ACGACGGCGC  ATACAATACC  GATATATTCA  ATAGTGTCAA
801 CGGCATCGAA  CGTGCTATC  TGCTACCCTC  CCTGAAGTCC  GGCATACGCC
851 GCATTTTCGT  CGTTGGATTG  AGTACAGGTT  CGTGGGCGCG  CGTCTTGTCT
901 GCCATTCCGG  AAATGCAGTC  GATGATCGTT  GCGGAAATCA  ATCCGGCATA
951 CCGTAGCCTT  ATCGCGGAcg  agccgcAAAT  CGCACCGCTT  TTGcAGGACA
1001 AACGTGTTGA  AATTGTATTG  GATGACGGTA  GGAAATGGCT  GCGTCGCCAT
1051 CCTGATGAAA  AATTCGACCT  GATTTTGATG  AATTCGACTT  GGTACTGGCG
1101 TGCCATTTC  ACTAACCTGT  TGAGTGCGGA  ATTTTAAAA  CAGGTGCAAA
1151 GCCACCTTAC  CCCGGATGGT  ATTGTAATGT  TTAATACCAC  GCACAGCCCG
1201 CATgctTTTG  CTACCGCCGT  ACACAGTATT  CCCTATGCAT  ACCGCTACGG
1251 GCATATGGTA  GTCGGCTCGG  CAACCCCGGT  AGTTTTcct  AATAAAGAAC
1301 TGCTCaagca  aCGCCTTtcc  cgGTTGATT  GGCCGGAAG  CGGCAGgcac
1351 gtATTGACA  GCAGACCGT  GGATGCTGCA  GCACAAAAG  TTGtctctCG
1401 TATGCTGATT  CGGATGACGG  AAcctTCGGC  TGGGGCGGAA  GTCATTACTG
1451 ACGATAATAT  GATTGTAGAA  TACAAATACG  GCAGAGGGAT  TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPN  SVINMLSFLT  GLLSLGIEVL  WVRMFSFAAQ  SVPQAFSFI
51  ACFLTGIAVG  AYFGKRICRS  RFVDIPFIQ  CFLWAGIADF  LILGAAWLLT
101 GFSGFVHHAG  IPITLSAVVR  GLIFPLVHHV  GTDGNKSGRQ  VSNVYFANVA
151 GSALGPVLIG  FVILDLLSTQ  QIYLLICLIS  AAVPLFCTLF  QKSLRLNAVS
201 VAVSLMFGIL  MFLLPDSVFQ  NIAGRPDRLI  ENKHGIVAVY  HRDGDKVYVG
251 ANVYDGAynt  DIFNSVNGIE  RAYLLPSLKS  GIRRIFVVLG  STGSWARVLS
301 AIPEMQSMIV  AEINPAYRSL  IADEPQIAPL  LQDKRVEIVL  DDGRKWLRRH
351 PDEKFDLILM  NSTWYWRAYS  TNLLSAEFLK  QVQSHLTPDG  IVMFNTTHSP
401 HAFATAVHSI  PYAYRYGHMV  VGSATPVVFP  NKELLKQRLS  RLIWPESGRH
451 VFDSSTVDA  AQKVVSRLI  RMTEPSAGAE  VITDDNMIVE  YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG  TGAACACTAA  ACCGAATACT  AGTTTGATT  ATATGCnTTC
51  TTTCTTAGC  GGCTTATTGA  GCTTGGGTAT  AGAAGTCTTG  TGGGTGAGGA
101 TGTTTTCGTT  CGCAGCACAG  TCCGTGCCTC  AGGCAATTTC  ATTTACCCTT
151 GCCTGTTTT  TGACCGGTAT  CGCCGTCGGC  GCGTATTTTG  GCAAACGGAT
201 TTGCCGCAGC  CGCTTGTGTG  ATATCCCTT  TATCGGGCAG  TGCTTCTTGT
251 GGGCGGGTAT  TGCCGACTTT  TTGATTTTGG  GTGCTGCGTG  GTTGTGACG
301 GGTTTTTCCG  GTTTCGTCCA  CCACGCCGGT  ATCTTCATTA  CCCTGTCTGC
351 CGTCGTCAsA  sGGTTGATT  TCCGCTCGT  ACACCATGTG  GGTACGGATG
401 GCAACAAATC  CGGACGACAG  GTTCCAATG  TTTATTTGCG  CAACGTTGCC
451 GGCAGTGCAT  TGGGTCCGGT  CCTATCGGC  TTTGTGATAC  TTGATTCTT
501 GTCCACCCAA  CAGATTtACC  TGCTCATCTG  TwTGATTtCT  GCTGCTGTCC
551 CTTTGTtTTG  TACACTGTTC  CAAAAAGTC  TCCGACTGAA  TGCAGTGTcG
601 GTAGCAGTTT  CCCTAATGTT  CGGCATCCTC  ATGTTCTYAC  TGCCGGATTc

```





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```

g402      |||||:|||||
          HRDGDKVVYGANVYDGAYNTDIFNSVNGIERAYLLPSLKSIGIRRFVVGVLSTGSWARVLS
          250      260      270      280      290      300

          310      320      330      340      350      360
m402.pep  AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          |||||
g402      AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          310      320      330      340      350      360

          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          :|||||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420

          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESGRHFVDSSTVDAAAQKVVSRLMIQMTEPSAGAE
          |||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESGRHFVDSSTVDAAAQKVVSRLMIRMTEPSAGAE
          430      440      450      460      470      480

          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGTACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTCGCG CAACGTGCC
451 GGCAGTGCA TGGGTCCGGT CCTATCGGC TTTGTGATAC TTGATTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTT CAAAAAGTC TCCGACTGAA TGCAGTGTCTG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TCGGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCATC TGCTACCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCCTG TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGATGGT ATTGTAATG TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACGCCGT ACACAGTATT CCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CGGCAGGCAC
1351 GTATTTGACA GCAGACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```

```

51 ACFLTGIAGV AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPEVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDLRI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSGWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK VQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSSTDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

## m402/a402 99.0% identity in 497 aa overlap

```

              10      20      30      40      50      60
m402.pep      MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSAAQSVPAFSTLACFLTGIAGV
              |||||
a402           MDIVNTKPNTSLIYMLSFLSGLLSLGIEVLWVRMFSAAQSVPAFSTLACFLTGIAGV
              10      20      30      40      50      60

              70      80      90      100     110     120
m402.pep      AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX
              |||||
a402           AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR
              70      80      90      100     110     120

              130     140     150     160     170     180
m402.pep      XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS
              |||||
a402           GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS
              130     140     150     160     170     180

              190     200     210     220     230     240
m402.pep      AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDLRIENKHGIVAVY
              |||||
a402           AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDLRIENKHGIVAVY
              190     200     210     220     230     240

              250     260     270     280     290     300
m402.pep      HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS
              |||||
a402           HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS
              250     260     270     280     290     300

              310     320     330     340     350     360
m402.pep      AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRHPDEKFDLILM
              |||||
a402           AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRHPDEKFDLILM
              310     320     330     340     350     360

              370     380     390     400     410     420
m402.pep      NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
              |||||
a402           NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
              370     380     390     400     410     420

              430     440     450     460     470     480
m402.pep      VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTDAAAQKVSRMLIQMTEPSAGAE
              |||||
a402           VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTDAAAQKVSRMLIQMTEPSAGAE
              430     440     450     460     470     480

              490
m402.pep      VITDDNMIVEYKYGRGIX
              |||||
a402           VITDDNMIVEYKYGRGIX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACAC TGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGCGG GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAGC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGRSSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSXGKIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACAC TGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTGCGACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAGC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK

```

729

```

51  DMDLQALHGR  KVALYIATMG  DQSGSGSLTGG  RYSIDALIRG  EYINSPAVRT
101 DYTYPREYET  AETTSGLTGG  LTSLSTLNA  PALSRTQSDG  SGSKSSLGLN
151 IGGMGDYRNE  TLTTNPRDTA  FLSHLVQTVF  FLRGIDVVSP  ANADTDVFIN
201 IDVFGTIRNR  TEMHLYNAET  LKAQTKLEYF  AVDRTNKKLL  IKPKTNAFEA
251 AYKENYALWM  GPYKVSIGIK  PTEGLMVDFS  DIRPYGNHTG  NSAPSVEADN
301 SHEGYGYSDE  VVRQHRQGPX  *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from

*N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRF AVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRF AVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
g406.pep	70	80	90	100	110	120
	KVALYIATMGDQSGSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG					
m406	KVALYIATMGDQSGSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG					
	70	80	90	100	110	120
g406.pep	130	140	150	160	170	180
	LTSLSTLNAPALSRTQSDGSGSRSS LGLNIGMGDYRNETLT TNPRDTAFLSHLVQTVF					
m406	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLT TNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
g406.pep	190	200	210	220	230	240
	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
g406.pep	250	260	270	280	290	300
	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
g406.pep	310	320				
	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC  GGCTGCTGAT  ACCTATTCTT  TTTTCAGTTT  TTATTTTATC
51  CGCTGCGGG  ACACTGACAG  GTATTCCATC  GCATGGCGGA  GGTAAACGCT
101 TC GCGGTCGA  ACAAGAACTT  GTGGCCGCTT  CTGCCAGAGC  TGCCGTTAAA
151 GACATGGATT  TACAGGCATT  ACACGGACGA  AAAGTTGCAT  TGTACATTGC
201 AACTATGGGC  GACCAAGGTT  CAGGCAGTTT  GACAGGGGGT  CGCTACTCCA
251 TTGATGCACT  GATTTCGTGG  GAATACATAA  ACAGCCCTGC  CGTCCGTACC
301 GATTACACCT  ATCCACGTTA  CGAAACCACC  GCTGAAACAA  CATCAGGCGG
351 TTTGACAGGT  TTAACCACTT  CTTTATCTAC  ACTTAATGCC  CCTGCACCTC
401 CGCGCACCCA  ATCAGACGGT  AGCGGAAGTA  AAAGCAGTCT  GGGCTTAAAT
451 ATTGCGGGA  TGGGGGATTA  TCGAAATGAA  ACCTTGACGA  CTAACCGCGG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC GACATAGACA
951 AGGCAACCT TGA

```

-- This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTG .LTTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEAN
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFFS DIQPYGNHMG NSAPSVEADN
301 SHEGYGSDE AVRRHRQGQP *

```

m406/a406 98.8% identity in 320 aa overlap

m406.pep	10	20	30	40	50	60
	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAANKDMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAANKDMDLQALHGR					
	10	20	30	40	50	60
m406.pep	70	80	90	100	110	120
	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPREYETTAETTSGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPREYETTAETTSGLTG					
	70	80	90	100	110	120
m406.pep	130	140	150	160	170	180
	LTTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	190	200	210	220	230	240
	FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	250	260	270	280	290	300
	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFSIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFSDIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
m406.pep	310	320				
	SHEGYGSDEVVRQHRQGQPX					
a406	SHEGYGSDEAVRRHRQGQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```

```

101  tcgtcaaacy attcggacac caagccgctg tctcggctga ggccgagggg
151  cagctgggtc atgtcggttc agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggc cagaccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgctgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttccgc tttcagttcg tcgtcttggt tgtcaaatc caacaaggct
701  ttcgggtgga tgcgatttgc gcggttgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgag agttcgggat
801  tgcgcagctt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901  atcgccctcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaatacccag ttcgcgcgcg
1001 atgatggcgg cgtggcaggc gcgtccgccg cggttggtca cgtggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggttaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatt tttaatcagg
1151 gcacacttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgagg tttgacggtt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtgcaa ctcggtgatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggtttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc ggggtgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLADT DIFVLLAAGG DGMQHHFDG RFAVVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGFVEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRCG VTGDAADNFR FQFVLFVKF QQGFVRDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDGDFGCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHGDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAAFLLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGFEBI KFRVRDRALY DVFAQTVRGG NKDDLTVVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggctcgac sggccttgac cgcagatgcc gacatatttg tctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgctg
101  tcgtcaaacy attcggatac caagccgctg tcgcggtcga gaccgagggg
151  cagttgggtc atgtcggttc agccgatgga gaagccgctg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301  gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggy caacccatt tcacgcgga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgctg gcgacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgccgc
501  cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttccgc ttttaattcg tcgtcttggt tgtcaaatc caacaargct

```

732

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca gggtggcgaa gctgaatcg agttcgggat
801 tgccgacgtt catcatgact tttacaggtg ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttcg gcacaggata cggttaacttc ttgaccgttt ttcagcaatt
951 cggttgcatg gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgccc cggttggtta cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgccgc cttcgcataa
1201 tacggttttg tcgcccgttg tggcgaagcg gcgcagggtg cggttgccct
1251 cttcttgagg ttttacgggt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgcaa ctcagtaatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttgggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatgggt ttacgcagga tggcgggctt gccggytttg agcgtgggtt
1551 tgaacacatr aaattcgtcc ggggtgaccg caccttgatc gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
  1  MVGXALTADA DIFVLLAAGG DGKVQHFDG RVAFVKRFGY QAAVAVETEG
 51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101  DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151  TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201  FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QQXFGVDTDL AVDDKFHTRQ
251  ADAFAGQVGE AECEFGIADV HHDFFRCFRH IVXGDIGNLY VQQTGIDKAG
301  IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351  STFHHGFPIR IGHVGNFYVA GFDGIHLGSI FNQAHALTD FLTDGAFAFX
401  YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451  PFDGQCVMRQ LSNFFVGNGE AVAVFLGDDI VGYFTGFCF VGKNHDFVFX
501  THGFTQDQGL ARFERGFEXH KFRVRDRTLY DVFAQTVRGG NKDDLIVXGF
551  GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
g501	MVGRTLTADTDIFVLLAAGGDGKMQHFDGRVAFVKRFGHQAAVSVEAEGQLGHVVRADG					
	10	20	30	40	50	60
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
g501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG					
	70	80	90	100	110	120
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRITTEAQHRVFFMRVYVAADQGVFGFVGVGH					
g501	QTHFVTNAFQGFQGETVFEALGNITRRITTEAQHRVFFMRVYAAADQGVFGFVGVGH					
	130	140	150	160	170	180
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
g501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
	190	200	210	220	230	240

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g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLFVKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	250 260 270 280 290 300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHDFYRCFRHIVXGDI GNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHDFDGC FWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	310 320 330 340 350 360
	IAFGTGYGNFLT V FQQFGC IAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
g501	IAFGTGYGNFLT V FQEFGR IAAADDGRNTQFARDDGGVAGASAAVGH DGGSTFHHGFPIR
	310 320 330 340 350 360
m501.pep	370 380 390 400 410 420
	IGHVGN EYVAGFDGIHLGSI FNQAHLALTDFLTDGA AFXYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAHLALTDFLTDGTTFAQDGF FAVDGVAAQVA AAFVFLG
	370 380 390 400 410 420
m501.pep	430 440 450 460 470 480
	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVRVVCQLGDF FVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	490 500 510 520 530 540
	VGYGFTGFCFVGKNHFDVFXTHGFTQDGG LARFERGF EHXKFVRVDRTLYDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGF EHKFVRVDRLYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	550
	NKDDLIVXGFGVGEHHT
g501	NKDDLIVVAGFGVGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

1	ATGGTCGGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGGCGGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTCGATAC	CAAGCCGCTG	TCGCGGTCGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTTCG	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA
201	GGAATTGTTC	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT
301	GACAACGGCT	TCGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTTGGT	CAACCCCAT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT
401	TCCAAGGCGA	AACAGTCTTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTTCTTCATG	CGGTTTCGTAT	ACGTTGCCGC
501	CGACCAGGTT	GGCGTATTCG	TTGGATTTGA	AGTCGGACAT	ACGGACGATG
551	GTTTTACGCG	GATAAACCGA	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGGCG	ATACGGCGGG
651	TAATTTCCGC	TTTAAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTTC	GCGGTTGATG	ATAAATTCCA	TACGCGCCAA
751	GCCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCGGGAT
801	TGCCGACGTT	CATCATGACT	TTTACAGGTG	CTTTAGGCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAAC TTC	TTGACCGTTT	TTACGCAATT
951	CGGTTGCATT	GCCGACGCCG	ACAACGGCAG	GAATACCCAG	TTCGCGCGCG



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```

1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGTT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTGCGACAA
1201 GACGGTTTTT TCGCCGTGA TAGAAAAGCG GCGCAGGTG CGGCTGCCTT
1251 CTTCTGGGA TTTGACGGT TCGGGACGGG CTTGCAGGAT GTAGAGTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGTTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGTAC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

```

a501.pep
1 MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRR
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFVVDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAFAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVNGE AVAVFFGDI VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTG
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTEAQHRVFFMRVYVAADQVGVFVGFVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTEAQHRVFFMRVYVAADQVGVFVGFVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFVVDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFVVDL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDDGGVAGTAAVGNDRSTFHHGFP					
a501	IAFGTGYGNFLTIVFQQFGCIAAADNGRNTQFARDDGGVAGTAAVGNDRSTFHHGFP					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGAA FAXYGFVAVDGEAAQVAVALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAY LALTD FLTDGAA FQDGF FAVDRKAAQVAAAF FLG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFVHRAAVVFFDGGCVMRQLGDFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
	490	500	510	520	530	540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFENXKFVRVDRTLVDVFAQTVRGG					
a501	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALVDVFAQTVGXS					
	490	500	510	520	530	540
	550	559				
m501.pep	NKDDLIVXGFGVEGEHHTX					
a501	DKDDLIVVTGFGIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctcgccgttt gctccctgac
51  cgtcgccgtc gcttcgcgac aggcggggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcgcca gcttcaccca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacgggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgcgccc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccg
451 ctaccaatac atccgcatcg gcttcaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51  SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RNAQTQQR
151 LPIHPHRLQR QPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctcgccgttt gctccctgac
51  cgtcgccgtc gcttcgcgac aggcggggcgc ggttagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcgcca gcttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgctc
251 gcgacgggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgcccgtta
451 ccaatacatc cgcacgggct tcaaaaggcg caacctcgcc gccatgcage
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQQRRL
151 PIHPHRLQR QPRRHAA

```

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLTPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

```

1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GCTCCCTGAC
51  CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGCGGCG AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG GGCAACGCCC AAACGCAACA ACGCCGGCTA
451 CCAATACATC CGCATCGGCT TCAAAGGCGG CAACCTCGCC GCCATGCAGC
501 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

```

1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51  SKKKKTQTAHG TFKILRPGLF KWEYTSPLYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV GNAQTQQRRL
151 PIHPHRLQRR QPRRHAA*

```

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSPLYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

## g502-1.seq

```

1 ATGatGAAAc cgcaCaacct gttccaatTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

## g502-1.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

## m502-1.seq

```

1 ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

## m502-1.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSIF GGLTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSSIF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSSIF					
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSSIF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSSIF					
	130	140	150	160	170	180

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```

          190      200
m502-1.pep  GGLNTNPQLSRGAFKFTPPKGV DVL SNX
            |||
g502-1      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTT GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51 SKKKTQTAHG TFKILRPLGF KWEYTSFYKQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

          10      20      30      40      50      60
a502-1.pep  MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG
            |||
m502-1      MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVOQSKKKTQTAHG
          10      20      30      40      50      60

          70      80      90      100     110     120
a502-1.pep  TFKILRPLGFKWEYTSFYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
            |||
m502-1      TFKILRPLGFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
          70      80      90      100     110     120

          130     140     150     160     170     180
a502-1.pep  ALESSYTLKEDGSSNGIDYVLATPKRNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
            |||
m502-1      ALESSYTLKEDGSSNGIDYVLATPKRNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
          130     140     150     160     170     180

          190     200
a502-1.pep  GGLNTNPQLSRGAFKFTPPKGV DVL SNX
            |||
m502-1      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgctcgcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaac cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

739

m503.seq  
 1 atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat  
 51 ttcggcatcg agctgttcgg ggaaggcgt atccaaaatc cattggcgga  
 101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt  
 151 gccagtgcgg cggaatgcg ttcgctcaga ccgttgtgtg cgaggaatgc  
 201 gcggtag

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

m503.pep  
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNNF  
 51 ASAAEMRSLR PLCARNAR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

m503/g503

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNNFASAAEMRSLR					
	:  :					
g503	MSAPSASVILFHAASISASSCSGKGVSKIHWRIPLTRASSETSTSNNFARAAEMRSFR					
	10	20	30	40	50	60

	69
m503.pep	PLCARNAR
g503	PLCARNAR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

a503.seq  
 1 ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT  
 51 TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA  
 101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT  
 151 GCCAGTGGCG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC  
 201 GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

a503.pep  
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNNF  
 51 ASAAEMRSLR PLCARNAR\*

m503/a503 100.0% identity in 68 aa overlap

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNNFASAAEMRSLR					
	:  :					
a503	MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNNFASAAEMRSLR					
	10	20	30	40	50	60

	69
m503.pep	PLCARNARX
a503	PLCARNARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

g503-1.seq  
 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT  
 51 AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA  
 101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG  
 151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTTC ATGCCGCTTC  
 201 GATTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGCCAAA ATCCATTGGC  
 251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGCTTTC GACATCCAAT  
 301 TTGCCCAGAG CGGCGGAAAT GCGTTCGTTC AGACCGTTGT GTCCGAGAAA  
 351 TGCGCGGTAG

740

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

## g503-1.pep

```

1  MARSLYREAK TWRI AFLTSL KPLIFRKVSC WPANDASGRS SAVAERTAT
51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FARAAEMRSF RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

## m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51 AACGTTATCC AAGCCGTTGA TGTTCAGAA GGTTCCTGT TGTCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTGTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

## m503-1.pep

```

1  MARSLYREAN TWCIASTLS KPLMFKKVSC CPANDASGRS SAVAERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRI	AFLTSLKPLIFRKVSCWPANDASGRSS	SAVAERTATEMSAPSASVI			
m503-1	MARSLYREANTWCI	ASLTLSKPLMFKKVSCCPANDASGRSS	SAVAERTATEMSAPPASAT			
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKI	HWISLPTRASSETSSSTSNFARAAEMRSFRPLCARNARX				
m503-1	ILFHAASISASSCSGKGVSKI	HWISLPTRASSATSSSTSNFASAAEMRSLRPLCARNARX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

## a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51 AACGTTTTTC AAGCCGTTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGCAGGTCT TCGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTGTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

## a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRI	ASLTFSKPLIFRKVSCWPANDASGRSS	SAVAERTATEMSAPPASAT			
m503-1	MARSLYREANTWCI	ASLTLSKPLMFKKVSCCPANDASGRSS	SAVAERTATEMSAPPASAT			
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKI	HWISLPTRASSATSSSTSNFASAAEMRSLRPLCARNARX				
m503-1	ILFHAASISASSCSGKGVSKI	HWISLPTRASSATSSSTSNFASAAEMRSLRPLCARNARX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```
g504.seq
1   atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgacacg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttggaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgtgta ccgcatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccctgt cgccgggtgc gcttttggtc tatctcggct cggtatgtgt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggctggtg
1151 tattgttttc aaacdgcaaa atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga
```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```
g504.pep
1   MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFAWNLK DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKES LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQODKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLQLDQ FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFVVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```
m504.seq..
1   atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgacacg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttggaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccggtttt gcaggacag gattattttt
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgtc gggtttgcag
```



742

```

1051 atgaccggtt ccccggtgc gcttttggtc tatctcggct cgggtgctgtt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggt
1151 tattgttttc agacggcaaa atccggtttg ccatgtcttc ggcccgagc
1201 gaacgggatt tgcagaagga atttccaaaa cagtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

```

m504.pep..
1  ILVQDLPFVEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLQLDGF SEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng)

from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPFVEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI					
	:					
g504	MLVQDLPFVEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGS DLTFKAWNLGDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	YQASFADGGS DLTFKAWNLGDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPVLQEQ					
g504	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSG LQQQYRWLRIP LDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
	:					
g504	DYFWITGTRSG LQQQYRWLRIP LDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQDKMQGYFYEMLYGVMNAALDETIR					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTRSPGALLV					
g504	RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTRSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					
	:       :       :					

743

g504 YLGSVLLVLGTVFMFYVPKKRAWLFSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK  
 370 380 390 400 410

m504.pep DLNHD  
 |||||  
 g504 DLNHD  
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq  
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAA AATTCCATAT  
 51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG  
 101 TAACGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC  
 151 CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA  
 201 CGGCGGTTG GATTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC  
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA  
 301 ATTGGCAAAC ACAATATATCG TCTGAGTTC GATCAGTTTA CTTCTATGAA  
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAGC CTGAAATCCA  
 401 CGCTGAACGA TGTCGCGGCC GTTACTCAGG AAGGTAAAA ATACACCAAT  
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT  
 501 CGAATATAAA AACTATATGC TGCCGGTTT GCAGGAACAG GATTATTTT  
 551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT  
 601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA  
 651 GTTTTGAAG GATGGGAAG GCGCAAACG TCTGGTTGCC GACGCAACCA  
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TCGGGAAC  
 751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT  
 801 TACGTCCAAT ATCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTCT  
 851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTGGATGA AACCATACGC  
 901 CCGTACGGCT TGCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT  
 951 GCTGCACAGT ATGGATGCGT ACACGGGTT GACCGAATAT CCCGCGCCTA  
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTGTCAG  
 1051 ATGACCGGTT CCCCGGGTGC GCTTTGGTC TATCTCGGCT CGGTGCTGTT  
 1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAA CGGGCGTGGG  
 1151 TATTGTTTTC AGACGGCAA ATCCGTTTTC CCATGTCTTC GGCCCGCAGC  
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG  
 1251 GCTCGCAAG GACTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep  
 1 ILVQDLPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN  
 51 HPLTLHGITI YQASFADGGS DLTFKAWN LG DASREPVLK ATSIHQFPLE  
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN  
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR  
 201 IPLDKQLKAD FEMALREFLK DGEGRKRLVA DATKGAPAEI REQFM LAEN  
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR  
 301 RYGLPEWQQD EARNRFLHS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ  
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWLFS DGK IRFAMSSARS  
 401 ERDLQKEFPK HVESLQRLGK DLNHD\*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPFEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN	HPLTLHGITI
a504	ILVQDLPFEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN	HPLTLHGITI
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGS	DLTFKAWN LG	DASREPVLK	ATSIHQFPLE	IGKHKYRLEF	DQFTSMNVED
a504	YQASFADGGS	DLTFKAWN LG	DASREPVLK	ATSIHQFPLE	IGKHKYRLEF	DQFTSMNVED
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKS	SLKSTLXD	RAVVTQEG	KKYNIG	PSIVYRIR	DAAGQAVEYK
						NYMLPVLQEQ

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```

|||||
a504 MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
      130      140      150      160      170      180

      190      200      210      220      230      240
m504.pep DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
|||||
a504 DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
      190      200      210      220      230      240

      250      260      270      280      290      300
m504.pep REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
|||||
a504 REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
      250      260      270      280      290      300

      310      320      330      340      350      360
m504.pep RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
|||||
a504 RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
      310      320      330      340      350      360

      370      380      390      400      410      420
m504.pep YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
|||||
a504 YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
      370      380      390      400      410      420

m504.pep DLNHDH
|||||
a504 DLNHDH

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1 atgtttcgtt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51 catcctgttg accgccctgc tcaaatgcct ctccctgctg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcgtt ttacctttta
151 aaggaaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttgaact tgcccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaa cggtacacgg ctgggaacac gtgcagcagg ctttggacaa
351 gggcgaaggg ctgctgttca tcacgcgcga catcggcagc tacgatttgg
401 gcggacgcta catcagccag cagcttccgt tccacctgac cgccatgtac
451 aagccgcca aaatcaaaag gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgcccaccgg catacaaggg gtcaaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaaccac
601 gtcccttctc cgcaggaagg cggcggcgtg tgggcggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccagcgg acaaggcttc
751 gtgttgaca tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1 MFRLQFRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHlafYLL
51 KEDRARIVAN MRQAGLNPD TQTKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAHVHWEH VQALDKGEG LLFITPHIGS YDLGGRIYSQ QLPFHLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDQGQF
251 VLHIRPVQGE LNGNKAHDAA VFNRTYEWI RRFPTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

745

m505.seq (partial)

```

1  GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCTTTGTC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAACGG TCAAAGCCGT TTTTGGGAA ACGGCAAAAG
251 GCGGTTTGA ACTTGCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTC AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTTGA
351 CAAACACGAA GGGCTGCTAT TCATCAGGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TCAGAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAAAATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGTGCGA ACGCCTGCCT GGCGGACAA
751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTCCGACG CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPDP KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	LPLSCLHTLGN	RLGHlafYLL	KEDRARIVAN
g505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	LSLCLHTLGN	RLGHlafYLL	KEDRARIVAN
	10	20	30	40	50	60
m505.pep	MRQAGLNPDP	KTVKAVFAET	AKGGLLELAPA	FFRKPEDIET	MFKAVHGWEH	VQQALDKHEG
g505	MRQAGLNPDP	QTVKAVFAET	AKGGLLELAPA	FFRKPEDIET	MFKAVHGWEH	VQQALDKHEG
	70	80	90	100	110	120
m505.pep	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAIK	IMQAGRVRGK	GKTAPTSIQG
g505	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAIK	IMQAGRVRGK	GKTAPTSIQG
	130	140	150	160	170	180
m505.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VWVDFGKPA	YMTLAAXLA	HVKGVKTLFF
g505	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VWVDFGKPA	YMTLAAXLA	HVKGVKTLFF
	190	200	210	220	230	240
m505.pep	CCERLPGGQG	FDLHIRPVQG	ELNGDKAHDA	AVFNRAEYW	IIRFPTHI	
g505	CCERLPGGQG	FDLHIRPVQG	ELNGDKAHDA	AVFNRAEYW	IIRFPTHI	
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

```
a505.seq
1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTT TCGCGAAACG GCAAAAGGCG
251 GTTTGGAAct TGCCCCGCG TTTTTCAGAA AACCAGGAAG CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAATAACCG CGCCTACCAG CATACAAGGG GTCAAAACAA
551 TCATCAAAGC CCTGCGTTTC GCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATGGCA CACGTCAAAG
701 GCGTGAAGAC CTTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

```
a505.pep
1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPTQYLF MYNRYKMP*
```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLELAPFAFRKPEDIETMFKAVHGEHVQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPFAFRKPEDIETMFKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGVRGKGTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGVRGKGTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVTLFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCERLPGGQGFDLHIRPVQELNGDKAHDAAVFNRAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

747

## m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CCGGTTTGAA
201 CCCGACCCC AAAACGGTCA AAGCCGTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAAC TCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCGCA AAATCAAAGC GATAGACAAA ATCATGCAGG CCGGACGGGT
501 TCGCGGCAAA GGAACAAACG CGCCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCC GCGGAAGCAA CCATCGTCTT GCCCGACCAC
601 GTCCCTCCCT CTCAAGAAGG CCGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CAGCTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CCGACAAGGT
751 TTCGATTGCG ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

## m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGLHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDLET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTSIGG VKQIIKALRS GEATIVLPDH
201 VPSPEGGE GVVWDFFGKPA YMTLAAKLA HVGKVKTLFF CCE RLPGGQGG
251 FDLHIRPVQ GELNGDKAHD AAVFNRNAEY WIRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPD PKTVKAVFAETAKGGLLELAPAFFRKPEDLETMPKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPD TQTVKAVFAETAKGGLLELAPAFFRKPEDLETMPKAVHGW EHVQQALDKHEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRVRGK GKTAPTSIGG					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAI DKIMQAGRVRGK GKTAPTSIGG					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPEGGE GVVWDFFGKPAYMTLAAKLAHVKGKVT LFF					
g505	VKQIIKALRSGEATIVLPDHVPSPEGGE GVVWDFFGKPAYMTLAAKLAHVKGKVT LFF					
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQGFV LHIRPVQGE LNGDKAHDAAVFNRNAEY WIRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGFV LHIRPVQGE LNGDKAHDAAVFNRNAEY WIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	299

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120

748

m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWGHEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWGHEHVQQALDKHEG
	70 80 90 100 110 120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPKIKAIDKIMQAGVRGKGKTAPTSTIQG
a505	LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPKIKAIDKIMQAGVRGKGKTAPTSTIQG
	130 140 150 160 170 180
m505-1.pep	VKQIIKALRSGEATIVLPDHVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
a505	VKQIIKALRSGEATIVLPDHVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
	190 200 210 220 230 240
m505-1.pep	CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
a505	CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGC CGCTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCGC TTGATTTTCA AAGGCGGTTC GCGGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGCG GGCCTTGTC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGCG GTAATTGAAC AAACGGGCTT GCAACATTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGGCT
651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTCA CCAAAAAACG
751 TTCGCCCGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGGG CTTCGGGCAG CAGCGTCCAG AAGTCCAGT TGTGTTGGC
901 GGAACGCATA TTGGTGC GATCGCGTTT GACGGCTTTG TTCAGGTGCG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACC CGGAT
1051 GTCGCGTTC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCGGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTGG TGATGTCGTG TGTTACGGTA AACGTACCGA ACGCGCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGGCGCGC CGTGTTCAT
1351 GGTGAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCTTT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEVV VIVLAVVPVC
51  RVAVDFQRRF GEVGLLLPLA EAVGVVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEEVFGLAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLVDH

```

m506.seq

1	ATGGCGGTA	TTGATGAAGT	CGGGCGCGTC	GCCCATTCGC	GCGGCGGTGT
51	TGCCGAACAA	TGCTGTTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGGTTGGC	TGAAATAGTC	GTCATCGTCT	TGGCGGTA	CCCAGTGTGC
151	CGCGTCGCGC	TTGATTTTCA	AAGCGGTTTC	GGCGAAATCg	GGTGTGTGCT
201	GCCATTGGCC	GAAGCTGTyG	GGTTCGTAGT	GCGGCGAGGT	GCGCyAGTTG
251	CCGTGCGCGC	GGCCTTGCCC	GTyGCGsTgr	TtTgCTGTgAA	CAsgGCAACG
301	CGGACGATTG	ACGGGAATTT	GGCGGAAGTT	TACGCCCCAA	CGGTAGCGTT
351	GTGCGTCGCG	GTAATTGAAC	AAACGCGCTT	GCAGCATTTT	ATCTsGGCTG
401	GCGCCGACAC	CGGGAATCGG	GTTGCTCGGT	GCGAAGGCGG	ATTGTCCAC
451	ATCGCGCAAG	AAGTTTTCGG	GATTGCGGTT	CTCAACCGGA	TGTAAGGTA
501	CTTTTTCGCG	GCTCGTCTCA	GGCATGACTT	GGATGTACAT	CGTCCATTTC
551	GGAAACTCGC	CGCGTTCGAT	GGCTTCsTAT	AAGTCGCGCT	GATGGCTTTC
601	GCGGTGTCG	GCGATGATT	TGCGGCTTC	TTCGTGTGTC	AGGTTTTTAA
651	TGCCTTGTG	GGTGCGGAAA	TGGAATTTCA	CCCCAAAACG	CTCGCGTGCT
701	TCGTTCCAGA	AGCTGTAGGT	ATGCGAACCG	AAGCGCTGCA	TATGGCCGTA
751	GCCGCGGGGG	ATGCGCGCGT	CGCTCATCAC	GATGTTAACT	TGGTGCAGTG
801	CTTCGGGCAG	CAGCGTCCAG	AAGTCCCAGT	TGTTTGTGGC	AGAGCGCATA
851	TTGGTGC	GGTCGCGTTT	GACGGCTTTG	TTCAGGTCGG	GGAACCTACG
901	CGGGTCGCGC	AGGAAGAAC	CGGGCGTGT	GTTGCGGACC	ACATCCCAGT
951	TGCCTTCTTC	GGTATAAAAT	TTCAAGGCAA	AACCGCGGAT	GTCGCGTCTT
1001	GCATCGGCTG	GCGCGCGTTC	GCTTCGACG	GTTGTGAAC	GTCGCGAACAT
1051	CTCGGTTTTT	TTGCGCACTT	CGCTGAAGAT	TCCTTTGGCG	TGCATACGGC
1101	GTTCCGGGAT	GACTTCGCGC	ACGAAGTCGG	CGAGTTTTTC	AGTCATCGCT
1151	CTTGTTCCCT	TTCTCAGGTT	GGTCAAATGG	GGGTAAACGG	CTTACAGTAC
1201	GATTTGGCGG	AAAGCGTATT	CGTAACCCGT	TTCTTGATTG	CAATAAATTT
1251	CTTGAATCGA	CATTTTATTT	CCCTTTTGTA	AAAACATG	ATGCGACTAT
1301	ACGCGCAAGAT	TTTCGCTATT	AA		

m506, per

1	MAVFDEVGRV	AHCGGGVAEQ	CLFLRVVHQV	EQGARLAEIV	VIVLAVVPVC
51	<u>RVAVDFQRRF</u>	<u>GESGLLLPLA</u>	<u>EAVGFVVRQA</u>	<u>AXVAVGAALP</u>	<u>VAXXAVNXAT</u>
101	RTIDGNLAEV	YAQTVALCVG	VIEQTRLQHF	IXAGADTGNE	VARCEGDLFH
151	IGEEVFGIAV	QLEFAHFNQR	IVFFRPNFGQ	VKRMIRYFFR	VCFRHDLVHV
201	RPRFKLAAFD	GFXFXVALMAF	AVUGDDDFGG	FVGQVFNALL	GAEMEFHPKT
251	LACFVPEAVG	MRTEAVHMAV	AGGDAVAVAH	DGNLVQCFCG	QRPEVPVVCG
301	RAHIGARVAF	DGFVQVGELT	RVAQEEHGRV	VADHIPVAFF	GIKFQGGTAD
351	VAFCI GCAAF	ACHGGETGBH	LGFADFADFD	FGAGVFGDVG	RYGKRTERAR
401	TFGVHTAFGD	DFAHEVFEQF	IQPQILRQQR	AARTGGQAVL	IVGNRRRAVHV
451	GQMGYRAFGD	SHRSCSFSQV	QGMGGKRLTV	RFGGKRI RNR	FLDCNKFLES
501	TFYFFPVKTM	DATIRODFRY	*		

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/q506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDQRRF					
	:     :       :       :					
g506	MAVFDEVGRIAHCGGGVVKQSLFLRVVHQVEQGARLAEVVIVLAVVPVCRVAVDQRRF					
	10	20	30	40	50	60



	70	80	90	100	110	120
m506 .pep	GESGLLLPLAEAVGFVVRQAA	XVAVGAALPVAXXAVNXATRT	IDGNLAEVYAQTVALCVG			
g506	GEVGLLLPLAEAVGFVVRQAA	VAVGAALSVALVAVNRATRT	IDGDLAEVHTQAVTLRVG			
	70	80	90	100	110	120
	130	140	150	160	170	180
m506 .pep	VIEQTRLQHFIXAGADTGNE	VARCEGGLFHIGEEVFGIA	VQLEFAHFNQRIVFFRPN	FGQ		
g506	VIEQTGLQHFIRARADTGNE	VARCEGGLFHIGEEVFGIA	VQLEFAHFNQRIVFFRPN	FGQ		
	130	140	150	160	170	180
	190	200	210	220	230	240
m506 .pep	VKRMIRYFFRVCFRHDL	DVHRPFRLA	AFDGFXXVALMAFAVVG	DDFGGFFVGQVFNALL		
g506	VKRMIRHFFGIGFRHDL	DVHRPFRELAALDGF	VQVALMAFAVVGDDF	CSFFVGQVFNPLL		
	190	200	210	220	230	240
	250	260	270	280	290	300
m506 .pep	GAEMEFHPKTLACFVPE	AVGMRTEAVHMAVAGG	DAVAHHDGNLVQCF	GQQRPEVPVVC		
g506	AAEMEFHPKTFARFVPE	AVGMRTEAVHMAVAGG	NTAVAHHDGNLVQ	GFGQQRPEVPVVC		
	250	260	270	280	290	300
	310	320	330	340	350	360
m506 .pep	RAHIGARVAFDGFVQ	GELTRVAQEEHGRV	VADHIPVAFFGIKFQ	GKTADVAFCIGCAAF		
g506	GTHIGARIAFDGFVQ	GEFARVAQEEHGRV	VADHIPVAFFGIEFQ	RKTADVAFRIGCAAL		
	310	320	330	340	350	360
	370	380	390	400	410	420
m506 .pep	ACHGGETGEHLGFFAD	FAEDFGAGVFGDVV	RYGKRTERARTFGV	HTAFGDDFAHEVGEFF		
g506	ACHGGETGEHLGFFAD	FAENFGAGVFGDVV	CYGKRTERARTFGV	HTAFGDDFAHEVGEFF		
	370	380	390	400	410	420
	430	440	450	460	470	480
m506 .pep	IQPQILRQQAARTGGQ	AVLIVGNRAVVHGM	GYRAFGGSHRSCS	SFSQVGQMGKKRLTV		
g506	IQPQILRQQGAARAGGQ	AVLIVGNRAVVHGM	GYGAFGGSHRSCS	SFSQVGQMGKKRLTV		
	430	440	450	460	470	480
	490	500	510	520		
m506 .pep	RFGGKRIRNRFLDCN	KFLESTFYFFPVK	TMDATIRQDFRY			
g506	RFGGKRIRNRFLDCN	KFLESTFYFFPAK	TMDAIRQDFRY			
	490	500	510	520		

a506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCGTC	GCCCATTGCG	GCGGCGGTGT
51	TGCCGAACAA	TGCGCTGATC	TGCGCGCTCT	TCATCAGGT	GAACAGGGCG
101	CGCGCTTGTC	TGA AATGTT	GTCATCGTCT	TGGCGAGTAGT	CCCACTGCGC
151	CGCGTCGCGG	TTGATTTTCA	AAGGCGGTTG	GCGCAAGTCG	GCGTCTGCT
201	GCCATTGGCC	GAAGCTGTTG	GGTTCGTAGT	GCGGCAGGCT	GCCGTAGTTG
251	CCGTCGCGCG	GTCCTTGTC	GTCGCGCTAG	TTGCTGTGAA	CAGGGCAACG
301	CGGACGGTTG	ACAGGGATTT	GGCGGAAGT	CACGCCCAAG	CGGTAGCGGT
351	GCGCGTCGCG	GTAA TTGAAC	AAACGCGCCT	GCAACATTTT	ATCTGCGGCTG
401	GCGCCGACAC	CGGGAACGAG	GTTGCTCGGT	GCGAAGCGTG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CAACTCGAAT	TCGCCCATT
501	CAATCAGCGG	ATAGTCTTTT	TTGCGCCAA	CTTTGGTCAA	GTCAAACGGA
551	TGATCAGGCA	CTTTTTCGCG	ATCGGCTTCA	GGCATCACTT	GGATGTACAT
601	CGTCCATTTC	GGAAACTCGC	CGCGCTCGAT	GGCTTCGTAC	AGGTGCGCGT

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCAAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACC GAGCCGTGCA
801 TATGGCGGTA GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGC GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGCG GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGCGA ACAGGCGCGC CGTTGTTTCAT
1351 GGTACAGATGG GTTACAGGGC ATTGGAGGT ANTATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVCG
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGAFAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAALDGFVQVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHDLVHRPFRKLAALDGFVQVALMAFTTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVCG					
a506	GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGKIFQGKTADVAFCIGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGKIFQGKTADVAFCIGCAAF					
	310	320	330	340	350	360
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
a506	IQPQILRQQRARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTCAGACGG
101 CCTTTGCGCT CTTCTGTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT
201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGAATTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATT
351 GCTGCTGCTC CTGCCGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTCG CCGTGGCGGA TTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLLFDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTAAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTTCTGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT
201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGCCTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAGCTCGGT
301 TTGTTTTCCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATT
351 GCTGCTGCTC TTGATGAATG CGTTGTAAGT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTQQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

```

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51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG  
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRLR CLLVAFDALV QVLLMADLFF  
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng)

from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVXGLVFLFQTTFALFVLGNRLFNGMGLKLLLRQFAAD					
	:         :         :         :         :         :					
g507	MLLPALQQGGGFLSGGGFGLVGVQGLVFLQTAFALFVLGNRLFNGMGLKLLLRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFDLQLVFFKLHADLLLL					
	:         :         :         :         :         :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	:     :         :         :         :         :         :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq  
 1 ATGCTCTTGC TGGCTTTGCA ACAAGGCGGC AGCTTCCTGC GCGGCGGGCG  
 51 TTTCGGCTTC GTCAGGCAGA TTCAGGGCTT GGTTTTCTCG TTTCAGACGA  
 101 CCTTTGCGCT CTTCTGTGCT GGCAACGGTT TGTTCCGCAT GGGCAAGCTG  
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT  
 201 GGGTTTGGA GGGCGCATG AGTGTGGCTT GGGTTTCTTC CAATTCGGGC  
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAATTCGGT  
 301 TTGCTTTTCT TCCGCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGATTT  
 351 GCTGCTGCTC CTGATGGATG CGCTGCATCT GCGCCTGCGC CGCCTGCTTG  
 401 TCGCGTTCGA TCGTGTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC  
 451 CAAACGGGCA ATCTGTTCCG CCAACACGCC GCGTTTGTG CCAATTCGT  
 501 GCACCGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG  
 551 TCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep  
 1 MLLALQGG SFLRGGGFGF VRQIQGLVFL FQTTFALFVL GNGLFMGKL  
 51 LLLQRQFAAD AVCLVLLGLE GGIECGLGFF QFGQTLFVFG NLHRPFRQFG  
 101 LLFFRLQLVF FKLHADLLLL LMDALHLRLR RLLVAFDALV QVLLMADLFF  
 151 QTGNLFAQHA AFVAQFVHRL LLRLFGSLQG VYFVV\*

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGVXGLVFLFQTTFALFVLGNRLFNGMGLKLLLRQFAAD					
	:         :         :         :         :         :					
a507	MLLLALQGGSFRLRGGGFGFVRQIQGLVFLFQTTFALFVLGNRLFNGMGLKLLLRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

754

```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
          70      80      90      100     110     120

          130     140     150     160     170     180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
          ||:| ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       LMDALHLRLRLRLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
          130     140     150     160     170     180

m507.pep  VYFVVX
          |||||
a507       VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGAG GGTGTGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCGA ATCTGCGCGA GTTTTCTCTG
151 CACGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGCGGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCATTGTC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTGG CTTCACACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFLL
51  HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVFL RVEFVDGDFG KPVLA VGFFQ GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGAG GGTGTGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGCGGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCAAGCTG
301 GGCATTGTC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTGG CTTCACACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51  HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLPAF LPVEGLLFKL
101 GDLLPVVFL LVEFVDGDFG KPVLA VGFFQ GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNDDV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLLQQGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFLFHNNIFFVQGL					
	:			:		:
g508	MVAFGVDQGLLLLQQGGLGGGLKLRQLGLQGLYAGVLLPALFLNLRFFLHGDVFFVQRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLAFLPVEGLLFLKGLDLPVVLFLLVFVDGDFG					
	: :			:		
g508	YGFQQLVELDVLVVLELGFIGEGKLLPAFLPVQGLLFEPGDLFPVVLFLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQQGLKRLFQTALLLLAAVRGGLLLVFEFGGFLQGNDDV					
				:		
g508	KPVLAVGFQQGLKRLFQTALLLLAAVRGGLLLVFEFGGFLQSSDDV					
	130	140	150	160		

```
a508.seq
  1  ATGGTAGCGT  TTGGCGTTGA  TCAGGGCTTC  CTGCTGCTGC  AACAGGGCGG
101  TTTGGGTGGC  GGCCTGACAC  TCGCGGACCT  TGGTTTGCG  GGTTTGTAGC
501  CGGGCGTATT  TTCTCCATAG  ATCTGCGCGA  GTTTCCTCTG
151  TACGACAATA  TATTCTTCGT  CCAAACCTCTG  TACGGCTTCG  CTCAACTCTT
201  CGAGCTTGAT  GFGCTGCTCG  TCGTTTTGGA  ACTCGGTTTC  ATAGGCGAGG
251  GCAAGCTCTT  GCTGGCGTTC  CTGCCAATCG  AAGGTTTGGT  GTTCAAGCTG
301  GGC AATTTGC  TGTTCGTAGT  TTTGTTTTTG  CTGGTTGAGC  TTGTGGACGG
351  CGACTTCGGC  AAGCCCGTAT  TGGCGGTTGG  CTTCCAACAG  GGCAAGCTGC
401  GCCTGTTTCA  GACGACCTTG  CTGCTCTTGG  CGGCTGTGCG  CGGCGGTTTG
451  CTGCTGGTGT  TCGAGTTCGG  CGGCGGCTTC  CTGCAAAATG  GCGATGTCGT
501  CTGA
```

a508.pep

1	MVAFGVDQGF	LLQQGLGG	GLKLRQLGLQ	GLYAGVLFPT	LLNLREFLL
51	YDNIFFVQTL	YGFAQLFDEL	VLLVLELGF	IGEGKLLAF	LPIEGLLFEL
101	GNLLLVLEL	LVELVDGDFG	KPVLAVGFQQ	GKRLRFQTL	LLAAVRGGL
151	LLVFEFGGGF	LONGDVV*			

	10	20	30	40	50	60
m508.pep	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFLLNHNIFVQGL					
a508	MVAFGVDQGGFLLLQQGGLGGGLKLRQLGLQGLYAGVLFPTLLNLRREFLLYDNIFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAFFFKLDVLLVVLELGFIGEGLKLLAFLPVEGLLFKLGDLLPVVLELLVEFVDGDFG					
a508	YGFAQLFELDVLVVLELGFIGEGLKLLAFLPIEGLLFKLGNNLLVVLELLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQQGKLRFLQTALLLAAVRGGLLLVFEFGGGLQGNDDVXX					
a508	KPVLAVGFQQGKLRFLQTLLLLAAVRGGLLLVFEFGGGLQGNDDVXX					
	130	140	150	160		

q509.seq

756

```

1  atgggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caagggcggt tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgctgtgtt gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggtcg
251 ccgttgtcga taaggggaac ttgcaatttt ttcaaatacat cgagaaattt
301 ttggggccga gcataaggct cgagaaagcc gaatttgag cccatgccca
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aaggttcttc ggtgcgggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggtatggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgctgcggta aaaacggaac
551 acggcatcgg cgtggcgggc gaaggcaaag cgagggttt cgccagaaac
601 aaacggattg ccgtcgcggc cgccgcggat ccagccgcgg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cacgcccgtt ttgatttcgt cgttgacgct gagtttgtgg cggcgcggtt
801 cgctggtctg ccacaagccc agaagcacgg tgcgatttc gcgcgcagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttcg gcagcagcg
901 gcggatgcgg cgttgaaat tcaaaacggc ttggcggtgc acttcggtcg
951 ggtgcgcggc caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgttttcga aaccaacggc gaggcttctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgcccgc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgatttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcc aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagtga acgccgccg acggcggtcg
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgccctt gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFAQCVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVDDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQOR
301 ADAAVEIQNG LALHFGRVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLR
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAAARRR
501 YNRPQLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLRRIGR RRPCFISPPR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTCGTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTTC
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGGGCAAG CAGACGGCTG
251 CCGTTGTGCA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGTT AGGGTTCTTC GCGCGGGCGG ATTTCTTCGT CGGGCGATTT
451 GTCGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCAGATT CGCCGCGATA GAAGCGGAAC

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757

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551  ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601  AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651  TGTCGGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701  TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751  CACGCCGTTG TTGATTTCGT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801  CGTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTtC GCgGCGCAGC
851  CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901  GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951  GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCCGTGC
1001 ACCGATTTCG CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTTCGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTTCGTCCA ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAAGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGCG GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAATTGCA TGATTTTCTT CTCTCGTCTG CCGTAAATAT
1401 TGTAAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTtCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTTGC TGCGGTACAG CCGCCACATC
1601 CTCTTGGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCGG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```

m509.pep
1   MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFAQCVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFEKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQDQSVDF AAQPCQRVGI GAAFALRQQC
301 ADAAVEAXDG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRAVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNAARRQ
501 RYNRPQLFFS EHHHDHRT RRCIPAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng)

from *N. gonorrhoeae*:

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
g509	MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFAQCVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTTLQFFQIIQKLLCRSIRLEKAFAAHTQTER					
g509	HVEAEHGHGTDEVCQTAFGKQAAAVVDKGTTLQFFQIEKFLGRSIRLEKAFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
g509	ARFAHSARHNVGNGAAVRFFGAGDFFVRRGCGCHYVVVDFDAADGKRQFAVKFVEFAAV					
	130	140	150	160	170	180



a509.seq

1	ATGGTCGCTG	TATGTGATGA	ACGGACTGTA	CAGTGGACGT	TGATGGCTCA
51	ATTCCGCGCAA	CAGGGCCGGT	TGTTTTTGCT	CTTCGTTGAG	GCTGTTGTAG
101	CTTTCCAAGC	CTGCGTGTTG	GAAAAGCTCG	GCAACCACAT	CGGCGTGTTT
151	GCTTCGCGTG	TGTCGCAAGT	CGAAGCGCAT	CATGTGGAAG	CGGAACACGG
201	ATACGGAACG	GATGAGGTCT	GCCAAACGCG	CTTCGGCAAG	CAGGCGCGTG
251	CGTTTGTCGA	TAAGGGAATG	TTGCAATTTT	TTCAATCAT	CGAGAAATTC
301	TTGTGCCGAA	GCATAAGGCT	CGAGAAGCG	GAATTTGCA	CCCATACCCA
351	AACCGGACGC	GCGCGCTTTG	CCCATGACGC	GCGCCATAAT	GTAGGCAATG
401	GCGCGACGGT	AGGGTTCCTC	GCGCGGGGCG	GTTTCTTCGT	CGGGCGATTT
451	GTCGGACAAC	GCCATCACAT	CGCCGTTGAC	TTTGACGCGG	CGGATGGAGA
501	GCGGCAGTTC	GCGGTAGAGT	TTGTGCGAGT	CGCCACGGTA	AAACCGGAAC
551	ACGGCATTCG	CGTGGCGGCG	GAAGGCAAAA	CGCAAGGTTT	CGGCAGAAAC
601	GAACGGAATG	CGCTCGCGGT	CGCCGCGCAT	CCACGCGCCG	ATTTTGAGGA
651	TGTCCGGAAC	GCGGACATCG	GGATAGGCCG	TCTGAAAGTC	GTGTTCCATC
701	TTGCGGTAGA	GCTTGGGCAG	GGCTTCAAAA	AAGTTCATCG	GAAAGATGGA
751	CACGCGCTTG	TTGATTTCTG	CGTTGACGCT	GAGTTTGTGG	CGGCGCGTTT
801	CGTGTGTTCT	GCACAAGCCC	AGCAGGATAG	TGTCGATTTC	CGGCGCGCAG
851	CGTGCCAGCG	CGTCCGCATT	GGTACAGCGT	TCCGCTTGCG	CGACGACGCG

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901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTCG CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTGGCGGC
1101 GCGTTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTTC AATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCGGCC AAAGCCGCGT CCTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTGT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACCTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCCTATCTC
1701 GCCGCTCCG GCATCGGCAC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```
a509.pep
1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVFOACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGNGATVGGF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKKAHRKDG
251 HAVVDFVDA EFVAARFAGL PQAQDSVDF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FEVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVAV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNVP QMPHPCQTVH TLTARVPKCR LKLNAARRQR
501 YNRPQLFXSE HHHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFRRAY
551 FGRRLRRFGC RXPCPISPLP ASAR*
```

m509/a509 93.0% identity in 575 aa overlap

```

      10      20      30      40      50      60
m509.pep  MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVFOACVLEKLGNHIGVFACVLAQVERH
          |||::|:| |||::|:| |||::|:| |||::|:| |||::|:| |||::|:|
a509      MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFOACVLEKLGNHIGVFACVLAQVERH
          10      20      30      40      50      60

      70      80      90     100     110     120
m509.pep  HVKAEHGYGTDEVCTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a509      HVEAEHGYGTDEVCTAFGKQAAAVVDKGM LQFFQIIIEKFLCRSIRLEKAEFAAHTQTER
          70      80      90     100     110     120

      130     140     150     160     170     180
m509.pep  ARFAHSARHNVDGAAVFFGAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||::|:| |||::|:| |||::|:| |||::|:| |||::|:| |||::|:|
a509      ARFAHSARHNVGNGATVGGFAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV
          130     140     150     160     170     180

      190     200     210     220     230     240
m509.pep  EAEHGIGVAAEGKAQGFGGRNKRIAVAVAADPAADFEDVRNADIGIRLKVVFHLAVELGQ
          ::|||::|:| |||::|:| |||::|:| |||::|:| |||::|:| |||::|:|
a509      KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIRLKVVFHLAVELGQ
          190     200     210     220     230     240

      250     260     270     280     290     300
m509.pep  GFKAHREDGHAVVDFVDAEFVAARFAGLPQAQDSVDFAAQPCQRVGIGAAAFALRQQC
          ||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a509      GFKKAHRKDGHAVVDFVDAEFVAARFAGLPQAQDSVDFAAQPCQRVGIGTAFALRQQR
          250     260     270     280     290     300

      310     320     330     340     350     360
```

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m509.pep	ADA	AVE	AXD	GLA	LHF	GRV	RQNG	NGN	GRIV	QLP	LHR	FAV	GFPR	FEP	PAD	GFR	QAA	FRAA	ASG																																								
a509	ADA	AVE	I	QD	GLA	LHF	GRV	RQNG	NGN	GRIV	QLP	LHR	FAV	GFPR	FEP	PAD	GFR	QAA	FRAA	ASG																																							
			310			320			330			340			350			360																																									
m509.pep	FFV	D	L	A	A	F	V	V	H	V	F	G	D	V	Q	N	L	G	E	Q	A	A	G	Q	X	I	V	G	L	F	V	Q	L	R	Q	Y	F	F	N	Q	C	R	A	V	V	G	S	G	Q	E	F	D	C	F	D				
a509	FFV	D	L	A	A	F	V	V	H	V	F	G	D	V	Q	N	L	G	E	Q	A	A	G	Q	X	I	V	G	L	F	V	Q	L	R	Q	Y	F	F	N	Q	C	R	A	V	V	G	S	G	Q	E	F	D	R	F	D				
			370			380			390			400			410			420																																									
m509.pep	NQ	R	R	G	F	F	V	Q	E	V	E	Q	G	L	F	Q	K	F	R	V	R	R	Q	S	R	V	L	W	I	V	Q	N	M	Q	L	H	D	F	S	L	S	S	A	V	N	I	V	N	V	P	Q	M	P	H	P	C	Q	T	V
a509	NQ	R	R	G	F	F	V	Q	E	V	E	Q	G	L	F	Q	K	F	R	V	R	R	Q	S	R	V	L	W	I	V	Q	N	M	Q	L	H	D	F	S	L	I	-	A	V	N	T	V	N	V	P	Q	M	P	H	P	C	Q	T	V
			430			440			450			460			470			480																																									
m509.pep	HT	L	T	A	R	V	P	K	C	R	L	K	L	N	A	A	R	R	Q	R	Y	N	R	P	Q	L	F	F	S	E	H	H	D	H	D	R	T	R	Q	R	R	C	I	P	A	A	V	Q	P	P	H	P	L	G	R	N	R	H	
a509	HT	L	T	A	R	V	P	K	C	R	L	K	L	N	A	A	R	R	Q	R	Y	N	R	P	Q	L	F	F	S	E	H	H	D	H	D	R	T	R	Q	R	R	C	I	P	A	A	V	Q	P	P	H	P	L	G	R	N	H		
			490			500			510			520			530			540																																									
m509.pep	R	R	A	E	T	F	R	R	A	Y	F	G	R	R	L	R	R	F	G	C	R	T	X	P	T	L	P	L	R	V	S	A	R	X																									
a509	R	R	A	E	T	F	R	R	A	Y	F	G	R	R	L	R	R	F	G	C	R	X	P	C	I	S	P	L	P	A	S	A	R	X																									
			550			560			570																																																		
m509.pep																																																											
a509																																																											
			540			550			560			570																																															

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggttattcct gcccgaagcg
51  ggatagtgcc ttttggcagg cgttgccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggtcg
151 tggacgacgt tgagcgcggc cataatgacg atttttcgc tgcgcgcgac
201 ggggccgct tcgcgatgg cttcggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgatg acttcgatgt agactgttc gatgtcatc ctttaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgccca gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPOGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFVDLF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTGCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCCGCGAC
201 GCGTCCGCTT TCGCGGATGG CTTGCGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 GCGGTGCAwG ACTTCsAtGT GGACTTGTTG GATGTTGATC CTTTAATCCT
351 TATTGCTGCG TTTCTTGCCA TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPOGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
g510	MPSRTPQGKRGYSCPKRDSA FQALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

1	ATGCCTTCGC	GGACACCGCA	GGGAAAAGG	GGTTATTCCT	GCGCCAAGCG
51	GGATAGTGCT	TTTGGCAGG	CGTTGTCCAT	ATCGGCTATT	TTACGCGCAA
101	AATCGCCGAT	TGCCAATCG	CCGCCGTTC	GGGAGGTTT	CAACAGGTCG
151	TGGACGACGT	TGAGCGCGG	CATAATGAC	ATTTTTCGC	TGTCCGCGAC
201	GCGTCCGCCT	TCGCGGATGG	CTTCGGCTTT	GCCGTTGAGC	ATCCGACTG
251	CCTGCAACAG	TGTGTCTTT	TCTTCTGCCG	GCGTGTGAC	GGTCAGCCGG
301	G.CGTGCATG	ACTTCGATGT	GGACTTGTT	GATGTTTCATC	CTTAATCCT
351	TATTGCTGCG	TTTCTGCCG	TTGGGGAGG	CGCGCTGCCA	GTGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FQALSISAI	LRAKSPIAKS	PPFREVFNR
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPTACNSVSF	SSAGVLTVSR
101	XVHDFDVL	FDVHPLILIAA	FPAVGGGALP	VR*	

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA FQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

1	atgaaagtgc	ttgttttagg	tgcgggtggt	gccggcgat	cctccgtgtg
---	------------	------------	------------	-----------	------------

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```

51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101  gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151  tataccacgc cttgggctgc acccggtatt ccgaccaaag cactgaaacg
201  gctgtttaaa agccatccgc ctttactgtt ccgccctgac ggcggcctgt
251  atcaaatcga atggctgtgg cggatgctgc aaaactgcac ggcaacgcgc
301  tatcaaatca ataaagagcg catggtcagg atttccgaat acagccgtga
351  aatgttccgc cgttttgaag cgcaaacgca catgaatttt gagggacgca
401  aaaaaggac gttgcagatt ttccgccaaa ccgaagaagt cgaagcggca
451  aaacaagaca ttgccgtttt ggaacgctac ggcgtgccgt accgccgtct
501  gaagcccgaa gaatgcgcag aattcgagcc tgcgtggca cgcgttaccg
551  ccaaaattgt cggcggtctg cacctgcctg cggatgcgac cggcgactgc
601  cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtacg
651  gttctacttc aaccaacca tcagccgcat cgaccacaac gggctgcgca
701  tcaaagccgt tgaaacgaaa caggcggtt tgaacagat gccgttgtct
751  gcgcgctcgg ctgcttcagc aggactgtgt tggcgcagtt ggatctcaat
801  ctgccattt atcccgtaa aggcatttcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

```

g512.pep
1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTPWAAFGI PTKALKRLFK SHPLLFRPD GGLYQIEWLW RMLQNCTATR
101  YQINKERMVR ISEYSREMF RFEAQTDMNF EGRKKGTLQI FRQTEVEAA
151  KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201  RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251  ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

```

m512.seq (partial)
1  ..GTTTGGAAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAATTT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101  GCCTGCACCT GCCTGCAGAT GCGACCGGCG ACTggCGCCT CTTCCTGAA
151  AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201  AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAAA ACCGTTGAAA
251  CCAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301  TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTTATCCC
351  GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

```

m512.pep (partial)
1  ..VLERYGVPYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQKEG VRFHFNQNIS RIDHNLRIK TVETKQGGGL QMPLSARSA
101  SAGRFWRWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

```

m512/g512

          10      20      30
m512.pep          VLERYGVPYRRLKPEECAEFEPALARVTAK
                   |||
g512      TDMNFEGRKKGTQIFRQTEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
          130      140      150      160      170      180

          40      50      60      70      80      90
m512.pep      IAGGLHLPADATGDWRLFTEENLYKLKQEKGVRFHFNQNISRIDHNLRIKTVETKQGGGLK
               :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g512      IVGGLHLPADATGDCRLFTENLYKLKQEKGVRFYFNQTISRIDHNLRIKAVETKQGGGLK
          190      200      210      220      230      240

          100      110      120
m512.pep      QMPLSARSAVASAGRFWRWSWISICPFIPSKAIP
               |||:|||||:|||||:|||||:
g512      QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```

250                      260                      270

```
a512.seq
1 ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
51 GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCACTGAC CGCGCCGAGG
101 GCGTACCACT GGAAACCAGT TTTGCCAACG CAGCCACGCT TTTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCCGCG
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCGTGCCGT ACCCGCCTCT
501 GAAGCCCGAA GAATGCCGAC AATTCCGAGC TGCCTGGCA CGCGTTACCG
551 CCAAATTGC CGCGCGCTG CACCTGCCCG CAGACGCGAC CGCGCACTGC
601 CCGCTCTTCA CTGAAACCT GTACAAATTG TGTCAAGAAA AGGGCGTACG
651 GTTTCATTT AACCAAACCA TCAGCCGCAT CGACCACAA GGGCTGCGCA
701 TCAAAACCGT TGAAACGAA CAGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCG CTGCTTCAGG AGGACGGTTT TGCGCGAAGT GGATCTCAAT
801 CTGCGCGATT ATCCCGTCAA AGGCTATTCC TTGA
```

a512.pep

1	MKVLVLGAGV	AGVSSAWYLA	EAGHEVTVID	RAEGVAMETS	FANAGQLSYG
51	YTPWPAAGI	PTKALKWLFK	SHPPLLFRPD	GSLYQIEWLW	QMLQHCTAAR
101	YQINKERMVR	MSEYSREMFR	RFEAQTGMNF	EGRKKGTLQI	FRQTKEVEAA
151	KQDIADVLR	GVPPYRRVLF	ECAEFEPALA	RVTAKIAGGL	HLPADATGDC
201	RLFTENLYKL	CQEKGVRFHF	NQTISRIDHN	GLRIKTVETK	QGGCLKQMPLS
251	ARSAASAGRF	WRKWISICRF	IPSKAIP*		

```

                                10      20      30
m512.pep                      VLERYGVYPYRLKPEECAEFEPALARVTAK
                                |||||
a512      TGMNFEGRKKGTLLQIFRQTKEVEAAKQDI AVLERYGVYPYRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep      IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGGLK
              |||||
a512      IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQITSRIDHNGLRIKTVETKQGGGLK
              190      200      210      220      230      240

                                100      110      120
m512.pep      QMPLSARSVASAGRFWRKSWISICPFIPSKAIPX
              |||||:|||||
a512      QMPLSARSAASAGRFWRKSWISICRFIPSKAIPX
              250      260      270

```

```
g513.seq
  1  ATGGGTTCGG  CGCCGAACGC  CGCCGCCGCC  GCCGAAGTGA  AACACCCTGT
51  TTCGCAAGGT  ATGATTCAAA  TGCTGGGCGT  GTTTGTCTGA  ACCATCATCG
101 TTTGTTCTTG  CACCGCCTTC  ATCATCTTGA  TTTACCAACA  GCCTTATGGC
151 GATTTGAGCG  GTGCGGCGCT  GAcgCAGGCG  GCGATGTGTA  GCCAAGTGGG
201 GCAATGGGGC  GCGGGTTTCC  TCGCCGTGTA  CCTGTTTATG  TTTGCCTTTT
251 CCACCGTTAT  CGGCAACTAT  GCCTATGCCG  AGTCCAACGT  CCAATTATC
301 AAAAGCCATT  GGCTGATTAC  CGCCGTTTTC  CGTATGCTGG  TTTTGGCGTG
351 GGTCTATTTC  GGCGCGGGTG  CCAATGTGCC  TTTGGTCTGG  GATATGGCTG
401 ATATGGCGAT  GGGCAGCTAT  CGGTGGATCA  ACCTCGTCGC  CATCTCGCGG
451 CTCTCGCCat  TGCGTTTAT  GCTCGTGC  GACCTACACC  CCAAGCTGAA
```

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501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep  
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq  
 1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT  
 51 TTCGAAGGT ATGATTCAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG  
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC  
 151 GATTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG  
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT  
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC  
 301 AAAAGCCATT GGCTGATTAC CGCGGTTTTT CGTATGCTGG TTTTGGCGTG  
 351 GGTCTATTTC GCGCGGTTG CCAATGTGCC TTGGTCTGG GATATGGCGG  
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCTGCTG  
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCCG GATTACACCG CCAAGCTGAA  
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep  
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILEM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQOPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGMQMLGVFVDTIIVCSCTAFIILIYQOPYGDLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```
1 ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51 CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACACCGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTGT TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTGGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTTTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTGAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTAAGCGGCG GTCTGATTTC
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCTT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTCTT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTCGCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep
1 MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLEFTVTTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGPA
101 VFWMWVTALI GMSSAFVESS LAQLEKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGVFEEA VQNTNIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VEVDTIIVCS CTAFLILIYQ QPYGDLGAA LTQAAIVSQV
351 GQWAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```

                                     10      20      30
m513.pep                               MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
                                     |||
a513      DAAAGLLGGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD
           260      270      280      290      300      310

           40      50      60      70      80      90
m513.pep      TIIVCSCTAFIILIYQ QPYGDLGSAALTQAAIVSQV GQWAGFLAVILFMFAFSTVIGNY
           |||
a513      TIIVCSCTAFIILIYQ QPYGDLGSAALTQAAIVSQV GQWAGFLAVILFMFAFSTVIGNY
           320      330      340      350      360      370

           100      110      120      130      140      150
m513.pep      AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL
           |||
a513      AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMMGIMAWINLVAILL
           380      390      400      410      420      430

           160      170      180      190
m513.pep      LSPLAFMLLRDYTAKL KMGKDPEFKLSEHPGLKRRIKSDVWX
           |||
```



a513                    LSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX  
                          440                    450                    460                    470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq  
 1 atggttcaaa tacaggttgt gcgcgcgcgc ggcgttgccc gtggtctgca  
 51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg  
 101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa  
 151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga  
 201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt  
 251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag  
 301 cccgcccga acggtggtat cgaagaggac ggggtagctg cctgtcggga  
 351 tgctgcggtt gccgagtcgg cgcaaatgac ggcgggcggc ggtttgaccg  
 401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtaacca  
 451 gtatgcgcgc tgcattccgt ttctgcggc ggcgacgacg ctgcaggaaa  
 501 tgctgtggtg cgtgctttgc cgggtgtcgg caaacaccgt ggtgttgccg  
 551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc  
 601 gatgcggctg tccgtgtcca acgctgcctg ttcgattgt tttgccaagc  
 651 cgacggcggc ttccgtatcc aaatccatt cgtggtaaa gtcggggctg  
 701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc  
 751 ttccgcggtg tggcgggcga tgcgcgcggc ggcgcggacg gtgtcgcgca  
 801 gggcttggtt ggagaagtcg cgggtgccgg cgcgcgcctt gcgtttgccg  
 851 acgtaaacgg taatgtccag cgatttgcct tgctggaact cgatttgttc  
 901 gatttcgccc aagcgacgc tgacgctttg tccgagcgat tgcgtgaagt  
 951 cggttcggc ggcggtcgg cccgctgctt ttgccaagtc gagegtgcgg  
 1001 cggcagaggt cgaggagttc ggaagcgggt tggttgaaca gcataacaat  
 1051 cttctcttgt ggagcgttgt ggcattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep  
 1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK  
 51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADVEVDQ  
 101 PARNGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP  
 151 VVALHSVFGV GDDAAGNAVV RALPVCCKTV GVAVNVVLVS GLHRRAFGVF  
 201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV  
 251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLELDF  
 301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEEVEF GSGVVEQHNN  
 351 LSWWSVVF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)  
 1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA  
 51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC  
 101 GCGCCGCGCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC  
 151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC  
 201 CGAGTCGGCG CAAAGTGC GGCGGCGCG TTTGACCGAT GGTTCGGGG  
 251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG  
 301 CATGCCGTTT TCGTCGGCG CAACGACGCT GCAGGAAATG CTGTGGTGGC  
 351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG  
 401 TAATGGCCGG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TGCGCTCATC  
 451 CTCGTTGAGG GCGGCTGTGT CGCATGTGTT TGCCAAGCCG ACGGCGGCTK  
 501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT  
 551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG  
 601 GCGGGCGATG TCGATGGCG CTTTGACGGT GTCTTGACAG GCTTTTTCGG  
 651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA  
 701 ATGTCCAGCG ACTTGTCTCT CTGGAACGCG ATTTGTTsGA TTTsGCCCCAG  
 751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG  
 801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGGCGCG GCAGAGGTCTG  
 851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA  
 901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFG VLQGFGEVG STGAFAFAD VNGNVQRLVL LELDLXDAQ
251 PHADALSQXF AEIGFGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng)

from *N. gonorrhoeae*:

m515/g515

```

m515.pep          10      20      30
                  GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                  ::| | | | | | | | | | | | | | | | | |
g515              30      40      50      60      70      80
AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA

m515.pep          40      50      60      70      80      90
VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
| | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
g515              90     100     110     120     130     140
VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA

m515.pep          100     110     120     130     140     150
GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRRAFGVFDALIL
| | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
g515              150     160     170     180     190     200
GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLVLSGLHRRRAFGVFDAAVR

m515.pep          160     170     180     190     200     210
VQGGFLFALFCQADGGXRIQIPFVVKVGADVDFCHQTGIGKSGATVFGGVAGDVGDFGDFGV
| | | | | | | | | | | | | | | | | | : | | : | | | | | | | | | | | | | |
g515              210     220     230     240     250     260
VQRCLFALFCQADGGFRIQIPFVVKVGADVLRHQLGVGKSGATVFGGVAGDVGGGADGV

m515.pep          220     230     240     250     260     270
LQGFGEVVGSTGAFAFADVNGNVQRLVLELDLXDAQPHADALSQXFAEIGFGGGCAR
| | : | | | | : | | | | | | | | | | | | | | | | | | : | | : | | | | |
g515              270     280     290     300     310     320
AQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLFDFAQAHADALSERFAEVGFGGGRAR

m515.pep          280     290     300
RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
| | | | | | | | | | | | | | | | | | : | |
g515              330     340     350
CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVAF

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGC CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCGG

```

551	TAAACGTATT	GGTAATGGCC	GGTTTGCACC	GCCGCGCCTT	CGGAGTTTTT
601	GATGCGCTCA	TCCTCGTTCA	GGGCGGCTTG	TTTCGATTGT	TTTGCCAAGC
651	CGACGGCGGC	TTCCTGATCC	AAATCCCAT	CGTGGTAAAG	GTCTGGGGTCG
701	CCGATGTGTT	GCGCCATCA	CTCGGGGTCG	GCAAGTCCGG	CGCAACCGTC
751	TTCGGCGGTG	TGGCGGCGCA	TGTCNNNNGC	GGGCGGACG	GTGTCGCGCA
801	GGGCTTGTT	CGAGAAATCG	GCGGTGCCGG	GCGGCGCTTT	GCGTTTGCCG
851	ACGTAAACGG	TAATGTCCAG	CGACTGTGCC	TGCTGAAACT	CGATTGTGTC
901	GATTTCGCCC	AGCCGCACGC	TGACGGCTTG	TCCCAATGAT	TCGCTGAAAT
951	CGGCTTCGGC	GCGCGTTGCG	CCCCTCGCTT	TTGCCAAGTC	GAGCGTGCGG
1001	CGGCACAGGT	CGAGGAGTTG	GGAAGCGGTG	TGGTTGAACA	GCATAGAAAT
1051	CTTTCTTGAT	GATGCTTTGC	GGCATTTTAA		

a515.pep

```

1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEIEA  FDNAVLNHEA  RCGGNAFRIK
51  IAAAERAGDV  REFFAQVEEIG  QDFFADAVDQ  ETALAEASA  GCEADVESDK
101  TARNGGIEED  GVVACRDAAA  AESAQSAAGG  GLTDGFGVAH  IRMAAGGIVP
151  VUNLHAFVFG  GNDAAAGNAV  RALPVCKGTV  GVAVNVLVMA  GLHRRAGVGF
201  DALILVQGGL  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251  FGGVAGDVXX  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RLVLKLLDLF
301  DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEEVEF  GSGVVEQHRN
351  LS*CFAAF*

```

```

m515.pep      10      20      30
               GKSGGCAFFAQQVEEIGQDFSADAVDQETALA
               ::| | | | | | | | | | | | | | | | | |
a515      AEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDVRFFAQQVEEIGQDFFADAVDQETALA
               30      40      50      60      70      80

               40      50      60      70      80      90
m515.pep      VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
               90      100     110     120     130     140

               100     110     120     130     140     150
m515.pep      GGIVPVVALHAVFVGNGDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      GGIVPVVALHAVFVGNGDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
               150     160     170     180     190     200

               160     170     180     190     200     210
m515.pep      VQGGFLFALFCQADGGKRIQIPFVKVGADVFCHQTGIGKSGATVFGGVAGDVGDFG
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VQGGFLFALFCQADGGFRIQIPFVKVGADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
               210     220     230     240     250     260

               220     230     240     250     260     270
m515.pep      LQGFGEVGSTGAFAFADVNGNVQRLVLLLELDLXDAQPHADALSQXFAEIGFGGGCAR
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLDFDAQPHADALSQXFAEIGFGGGCAR
               270     280     290     300     310     320

               280     290     300
m515.pep      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
               | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
               330     340     350     360

```

g515-1.seq

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCC GTGGTCTGCA

```

51  TTCGAGTTT  GCGCGCGCTG  TAACTGCCGA  GGAAATAGCC  TTCGACAATG
101  CCGTTTTGAA  TCACGAAGCG  CGGCGCGGTG  GCAACACCTT  CCGCATCAAA
151  ATAGCTGCTG  CGGAAAGAGC  GGGGGATGTG  CGGTTCTTCG  CGCAGGTTGA
201  GGAAATCGGG  CAGGACTTTT  TTGCCGATGC  TGTCGATCAG  GAAACTGCTT
251  TGGCGGTAGA  GCGCGCCGCC  GGAGAGTGTG  CCGACGAGGT  GTCCGATCAG
301  CCGCGCCGAA  ACGGTGGTAT  CGAAGAGGAC  GGGGTAGCTG  CCTGTCCGGA
351  TGCTGCGGCT  GCCGAGTCGG  CGCAAAGTGC  GCGGGCGCGC  GGTTTGACCG
401  ATGGTTTCGG  GGCTGTCCAT  ATCCGGATGG  CGGCAGGCGG  AATCGTACCA
451  GTAGTCGCGC  TGCATTCCGT  TTTCGTGCGC  GGCAACGACG  CTGCAGGAAA
501  TGCTGTGGTG  CGTGCTTTGC  CGGTGTGCGG  CAAAACCGTG  GGTGTGCCG
551  TAAACGTATT  GGTAGTGTC  GGTGTGCACC  CGCGCGCCTT  CGGAGTTTTC
601  GATGCGGCTG  TCCGTGTCCA  ACGCTGCCTG  TTCGATTGT  TTTGCCAAGC
651  CGACGGCGGC  TTCCGTATCC  AAATCCCAT  CGTGGTAAAG  GTCGGGGTCG
701  CCGATGTGTT  GCGCCATCAA  CTCGGGGTCG  GCAAGTCCGG  CGCAACCGTC
751  TTCGCGGTG  TGGCGGGCGA  TGTCGGCGGC  GCGCGGACG  GTGTCGCGCA
801  GGGCTTGTTC  GGAGAAGTCG  CGGTGCGCG  CGCGGCCTTT  GCGTTGCGG
851  ACGTAAACGG  TAATGTCCAG  CGATTGTCC  TGCTGGAAGT  CGATTGTTC
901  GATTTGCGCC  AAGCGCACGC  TGACGCTTTC  TCCGAGCGAT  TCGCTGAAGT
951  CGGCTTCGGC  GCGGTGCGC  CCCGCTGCTT  TTGCCAAGTC  GAGCGTGCGG
1001  CCGCAGAGGT  CGAGGAGTTC  GGAAGCGGTG  TGGTTGAACA  GCATAACAAT
1051  CTTTCTTGGT  GGAGCGTTGT  GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

**g515-1.pep**

```

1  MVQIQVVRAA  GVARGLHSEF  ARAVTAEEIA  FDNVLNHEA  RRGNTFRIK
51  IAAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERAA  GECADEVSDQ
101  PARNGGIEED  GVAACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHSVFVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVVS  GLHRRAFGVF
201  DAAVRVQRCL  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251  FGGVAGDVGG  GADGVAQGLF  GEVGGAGAAF  AFADVNGNVQ  RVLLELDLF
301  DFAQAHADAL  SERFAEVGFG  GGRARCFQV  ERAAAVEEF  GSGVVEQHNN
351  LSWWSVVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

**m515-1.seq**

```

1  ATGGTTCAAA  TACAGTTGT  GCGCGCCGCC  GCGGTTGCCC  GTGGTCTGCA
51  TACCGAGTTT  GCGCGCGCTG  TAACTGCTGA  GGAAATAGCC  TTCGACAATG
101  CCGTTTTGAA  TCACGAAGCG  CGGTGCGGTG  GCAACGCCTT  CCGCATCAAA
151  ATAGCTGCTG  CGGAAAGAGC  GGGGGATGTG  CGGTTCTTCG  CGCAGGTTGA
201  GGAAATCGGG  CAGGACTTTT  TTGCCGATGC  TGTCGATCAG  GAAACTGCTT
251  TGGCGGTAGA  GCGCGCCGCC  GGAGAGTGTG  CCGACGAGGT  GTCCGATAAG
301  ACCGCGCGAA  ACGGTGGTAT  CGAAGAGGAC  GGGGTAGCTG  CCTGTCCGGA
351  TGCTGCGGCT  GCCGAGTCGG  CGCAAAGTGC  GCGGGCGCGC  GGTTTGACCG
401  ATGGTTTCGG  GGCTGTCCAT  ATCCGGATGG  CGGCAGGCGG  AATCGTACCA
451  GTAGTCGCGC  TGCATGCCGT  TTTCGTGCGC  GGCAACGACG  CTGCAGGAAA
501  TGCTGTGGTG  CGTGCTTTGC  CGGTGTGCGG  CAAAACCGTG  GGTGTGCCG
551  TAAACGTATT  GGTAATGGCC  GGTTCGACC  CGCGCGCCTT  CGGAGTTTTC
601  GATGCGCTCA  TCCTCGTTCA  GGGCGGCTTG  TTCGATTGT  TTTGCCAAGC
651  CGACGGCGGC  TTCCGTATCC  AAATCCCAT  CGTGGTAAAG  GTCGGGGTCG
701  CGATGTGTT  TTGCCATCAG  ACAGGCATCG  GCAAGTCCGG  CGCAACCGTC
751  TTCGCGGTG  TGGCGGGCGA  TGTCGATGGC  GGCTTTGACG  GTGCTTGCA
801  GGGCTTTTTC  GGAGAAGTCG  GCAGTACTGG  CGCGGCCTTT  GCGTTTGCCG
851  ACGTAAACGG  TAATGTCCAG  CGACTTGTC  TGCTGGAAGT  CGATTGTTC
901  GATTTGCGCC  AGCCGCACGC  TGACGCTTTC  TCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

**m515-1.pep**

```

1  MVQIQVVRAA  GVARGLHTEF  ARAVTAEEIA  FDNVLNHEA  RCGNNAFRK
51  IAAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERAA  GECADEVSDK
101  TARNGGIEED  GVAACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHSAFVG  GNDAAAGNAV  RALPVCCKTV  GVAVNVLVMA  GLHRRAFGVF
201  DALILVQGL  FALFCQADGG  FRIQIPFVVK  VGVADVFCQ  TGIGKSGATV
251  FGGVAGDVGG  GFDGVLQGF  GEVSGTAAAF  AFADVNGNVQ  RLVLELDLF
301  DFAQPHADAL  SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNVLNHEARRGGNTFRIKIAAAERAGDV
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNVLNHEARRCGNNAFRKIAAAERAGDV
          10      20      30      40      50      60

```

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSHVFGGNDAAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSHVFGGNDAAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLVVSGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVADVLRHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

1	ATGGTTCAAA	TAAAGTTGT	GCGCGCCGCC	GGCGTTGCCC	GTGGTCTGCA
51	TTCCGAGTTT	GCGCGCGCTG	TAACTGCTGA	GGAAATAGCC	TTCCGACAATG
101	CCGTTTTGAA	TCACGAAGCG	CGGTGCGGTG	GCAACGCCCT	CCGCATCAAA
151	ATAGCTGCTG	CGGAAAGAGC	GGGGGATGTG	CGGTTCTTCG	CGCAGGTGTA
201	GGAAATCGGG	CAGGACTTTT	TTGCCGATGC	TGTCGATCAG	GAAACTGCTT
251	TGGCGGTAGA	GCGCTCCGCC	GGAGAGTGCG	CCGACGAGGT	GTCCGATAAG
301	ACCGCCCGAA	ACGGTGGTAT	CGAAGAGGAC	GGGGTAGTTG	CCTGTCGGGA
351	TGCTGCGGCT	GCGAGTCCG	CGCAAAGTGC	GGCGGGCGGC	GGTTTGACCG
401	ATGGTTTCGG	GGCTGTCCAT	ATCCGGATGG	CGGCAGGCGG	AATCGTACCA
451	GTAGTCGCGC	TGCATGCCGT	TTTCGTCCGC	GGCAACGACG	CTGCAGGAAA
501	TGCTGTGGTG	CGTGCTTTCG	CGGTGTGCGG	CAAAACCGTA	GGTGTGCCG
551	TAAACGTATT	GGTAATGGCC	GGTTTGACCC	GCCGCGCCTT	CGGAGTTTTC
601	GATGCGCTCA	TCCTCGTTCA	GGCGGCGTTG	TTCGCATTGT	TTTGCCCAAGC
651	CGACGGCGGC	TTCCGTATCC	AAATCCCAT	CGTGGTAAAG	GTGCGGGTCG
701	CCGATGTGTT	GCGCCATCAA	CTCGGGGTCG	GCAAGTCCGG	CGCAACCGTC
751	TTGCGCGGTT	TGGCGGGCGA	TGTCGGCGGC	GGCGCGGACG	GTGTCGCGCA
801	GGGCTTGTTT	GGAGAAATCG	GCGGTGCCGG	CGCGGCCTTT	GCGTTTGCCG
851	ACGTAACCGG	TAATGTCCAG	CGACTGTGCC	TGCTGAAACT	CGATTTGTTT
901	GATTTCGCCC	AGCCGCACGC	TGACGCTTTG	TCCCAATGA	

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

1	MVQIKVVRAA	GVARGLHSEF	ARAVTAEIEA	FDNAVLNHEA	RCGGNAFRIK
51	IAAAERAGDV	RFFAQVEEIG	QDFFADAVDQ	ETALAVERSA	GECADDEVSDK
101	TARNGGIEED	GVVACRDAAA	AESAQSAAGG	GLTDGFGAVH	IRMAAGGIVP
151	VVALHAVFVG	GNDAAAGNAV	RALPVCCKTV	GVAVNVLVMA	GLHRRAFGVF
201	DALILVQGG	FALFCQADGG	FRIQIPFVVK	VGVDVLRHQ	LGVGKSGATV
251	FGGVAGDVGG	GADGVAQGLF	GEIGGAGAAF	AFADVNGNVQ	RLVLLKLDLF
301	DFAQPHADAL	SQ*			

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEIEAFDVAVLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDVAVLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

Seq	1	atgttggttc	gtaaaacgac	cgcgcgcgtt	ttggcggcaa	ccttgatact
51	gaacggctgt	acgatgatgt	tgcgggggat	gaacaacccg	gtcagcctaa	
101	caatcaccgc	caaacacggt	gacaaagacc	aaatccgcgc	cttcggtgtg	
151	gttgccgaag	acaatgccca	attggaanaa	ggcagcgtcg	ttgatgatgg	
201	cgggaataat	tggttcgcgc	tcaatccccg	agattccggc	aagctgacgg	
251	gccttttgaa	ggccggggtg	gacaagccct	tccaaatagt	tgaggatacc	
301	ccgagctatg	cccgccacca	agccctgcgc	gtcaaattcg	aagcgcgccg	
351	cagccagaat	ttcagtaccg	gaggtctttg	cctgcgctat	gataccggca	
401	gacctgacga	catcgccaag	ctgaaacagc	ttgatgttaa	agcggtcaaa	
451	ctcgacaatc	ggacatttta	cacgcgcgtc	gtatccgcga	agggcaataa	
501	ctacgcacgc	ccgcaaaaac	tgaacgcgca	ttatcatttt	gagcaaagtg	
551	tgcccgccga	tatttattat	acggttactg	aaaaacatac	cgacaaatcc	
601	aagctgtttg	gaaatatctt	atatacgccc	cccttgttga	tattggatgc	
651	ggcggcccg	gtgctggctc	tgcctatggc	tctgattgca	gccgcgaatt	
701	ctctacagaca	atga				

1	MLFKRTTAAV	LAATLILNGC	TMMLRGMNPN	VSQITIRKHV	DKDQIRAFGV
51	VAEDNAQLEK	GSLVMGGKY	WFAVNPEDSA	KLTLGLKAGL	DKPFQIVEDT
101	PSYARHQALP	VKFEAPGSQN	PSTGGLCLRY	DTGRPPDIAC	LKQLEFKAVK
151	LDNRNIIYTRC	VSAGKYYAT	FQKLNADYHF	EQSVPADIIY	TVTEKHTDKS
201	KLFGNIIYTP	PLILIDAAAA	VLVLPMALIA	AANSSDK*	

1	ATGTTGTTCC	GTA AACGAC	CGCCGCCGTT	TTGGCGGCAA	CCTTGATGCT
51	GAACGGCTGT	ACGTTGATGT	TGTGGGGAAT	GAACAACCCG	GTCAGCGAAA
101	CAATCACCCG	CAAAACCGTT	GACAAAGACC	AAATCCGCGC	CTTCGGTGTG
151	GTGTCGCGAAG	ACAATGCCCA	ATTGGAAAGG	GGCAGCTCTG	TGATGTATGG
201	CGAAAATATC	TGGTTCTGTC	TCAATCCCGA	AGATTCGCGC	AGACTGACGG
251	GCATTTTGAA	GGCAGGGCTG	GACAAACCTT	TCCAAATAGT	TGAGGATACC
301	CCGAGCTATG	CTCGCCACCA	AGCCTGCGCG	GTCAAACCTG	AATCGCCTGG
351	CAGCCAGAAT	TTCAGTACC	AAGGCGCTTG	CCTGCGCTAC	GATACCGACA
401	AGCCTGCCGA	CATCGCCAA	CTGAACACG	TCGGGTTTGA	AGCGCTCAAA
451	CTCGACAATC	GGACCAATTA	CACGCGCTGC	GTATCCGCGA	AAGGCAATA

```
m516.ppep
  1  MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WVVNPEDSA KLTGILKAGL DKPFQIVEDT
101 PSYARHQALP VKLESPGSQN FSTEGLCRLY DTDKPADIAK LKQLGFVAVK
151 LDNRTIYTRC VSAKGQSYAT POKLNADYHF EQSVPADIYY TVTEEHTDKS
201 KLFAMILYTP PFLILDAAGA VLALPAAALG AVVDAARK*
```

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKQIRAFGVVAEDNAQLEK					
g516	MLFRKTTAAVLAATLILNGCTMMLRGMNPNVSTITRKHVDKQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSGQN					
g516	GSLVMMGGKYWFVAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSGQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m516.pep	FSTEGLCLRYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHFF					
g516	FSTGGLCLRYDTGRPDDIAKLKQLEFKAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHFF					
	130	140	150	160	170	180
	190	200	210	220	230	239
m516.pep	EQSVPADIIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIIYYTVTEKHTDKSLFGNIIYTPPLLIDAAAVALVLPMALIAAANSSDK					
	190	200	210	220	230	

```
a516.seq
1  ATGTTGTTCC GTAAACGCAC CGCCGCCGTT TTGGCGGCCAA CCTTGATGTT
51  GAACGGCTGT ACGGTAAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGGAAATAC TGGTTCGTCG TCAATCTCTGA AGATTGCGCG AAGCTGACGG
251 GCATTTTGAA GGCCGGGGTG GACAAGCAGT TTCAATATGT TGAGCCCAAC
301 CGCGCTTTTG CTTACCAAGC CCTGCCGGTC AAATCTGAAT CGCCCGCCAG
351 CCAGAATTTT AGTACCGAAG GCCTTTGCCT GCGCTTACGAT ACCGACAGAC
401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTCGAACTC
451 GACAAATCGA CCATTTACAC CGCGTGCCTG TCCGGCAAA GCGAAATACTA
501 CGCCACACCG CAAAACTCTG ACGCGGATTA TCATTTTGAG CAAAGTGTGC
551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
601 TTGTTTGAAA ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT
651 GCGCGCGGTG CTGGCCTTGC CTGTGCGGCG GTTGATTGCA GCCACGAATT
701 CCTCAGACAA ATGA
```

a516.pcp

773

```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKQFQMVPEP
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVPADIIYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHV	DKDQIRAFGVVAEDNAQLEK				
a516	MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHV	DKDQIRAFGVVAEDNAQLEK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDT	PSYARHQALPVKLESPGSON				
a516	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKQFQMVPEP	NRFA-YQALPVKLESPASQN				
	70	80	90	100	110	
	130	140	150	160	170	180
m516.pep	FSTEGLCRLRYDTDKPADIACLKQLGFEAVKLDNRTIY	TRCVSAKGKYATPQKLNADYHF				
a516	FSTEGLCRLRYDTRPADIACLKQLEFEAVELDNRTIY	TRCVSAKGKYATPQKLNADYHF				
	120	130	140	150	160	170
	190	200	210	220	230	239
m516.pep	EQSVPADIIYTVTEEHTDKSKLFANILYTPPFLILDA	AGAVLALPAAALGAVVDAARKX				
a516	EQSVPADIIYTVTKKHTDKSKLFENIAYTPTTLILDA	VGAVLALPVAALIAATNSSDKX				
	180	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

g517.seq

```

1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 cgggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatccccgatt tgatgttttt gggcaggctc atttggctgg
201 tgtcgccggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaaac
251 attttcattt gttcgggctt ggtgttttgc gcttcgctga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcataa ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag gggctgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1436; ORF 517.ng&gt;:

g517.pep

```

1  MHRVSDGIGV SVVFCRFVGF DDFLHQRMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAHI GERGDFNQAF FNQLGYTVKA HQVIEGLIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

m517.seq

```

1  ATGCATCGGG TTTCCAGACGG CATTTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCOA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```



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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep  
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT  
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ  
151 VSGQEAQFLA GFDGWAH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	:     :     :     :     :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	:     :     :     :					
g517	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLTGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq  
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT  
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG  
101 CCGGTAAAGG TGTGAAATA CAGCCCTCC ACGCCGTGCA GTTCTCAGC  
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG  
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTACGGAAC  
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA  
301 TCGCGCCGTT AGCGTCTTGC CGGCGATATA GGCAGAGCGG GCAATCTCAA  
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTGGAAGCC CATCAGGTCA  
401 TAGAGGGCAT CATAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG  
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep  
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT  
51 RIF\*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ  
151 VTGQKTQFLA GFDGRPH\*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	:     :     :     :     :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPDNVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLNQTF					

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```

              70      80      90      100      110      120
              130      140      150      160
m517.pep      FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX
              ||||| ||:|||||:|||||:|||||:||||| ||
a517          FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX
              130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1  atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttgtgtct
51  ttccgcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac ctttttttca gcataaatat tctgaccgga
151 agagcggcat ctccacgggc aaccgtgttc agactgcatc aggcggtacg
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcggcaaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1  MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKKSDFPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TTCGCAGGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCCTGTTC AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCGC TAGAACTAC GCCGTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPOATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRRERR RCVILSNGR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
g518          MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
              10      20      30      40      50      60

              70      80      90      100      110
m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHNRLPSAAGLVRRERRRRCVILSN
              | ||| || : :||| | ||||| ||| |||||
g518          RLHQAVRFHKMPKTISKMRNRYAVRITPPPRATLHYNRLPL-----
              70      80      90      100

m518.pep      120      130
              GRKKSDFPAFVAESEI
              |||||
g518          --KKSDPAFVAESEI
              110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 ..... .AAAAAAT CAGACCCTGC TTTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*

m518/a518  79.9% identity in 134 aa overlap

              10      20      30      40      50      60
m518.pep    MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
              |||||  || : |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a518         MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
              10      20      30      40      50      60

              70      80      90      100     110     119
m518.pep    RRHQA-RFARCRITINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG
              ||||  || : |||||  |||||  |||||  |||||  |||||  |||||  |||||
a518         RRHQAVRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-----
              70      80      90      100

m518.pep    120      130
              RKKSDPAFVAESEIX
              |||||  |||||  |||||  |||||
a518         -KKSDPAFVAESEIX
              110
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcattcccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgcctcg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcggy ggcttggggt
451 gtgaaagtcc tcggttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcy tccaatgccg agaaaaatcg ccgcatcaac cgcgccaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggtattaag cccgccaagg ttgccgaaat cgggaaccct
901 aattttcggc ggcattgaaa attttcgcca gaagcaaaaa cggccaataa
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

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101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAAN  
 251 RQIAAALQTO SGADAVNLKI AGQYVTAFAKN LAKEDNTRIK PAKVAEIGNP  
 301 NFRRHEKFSP EAKTAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)  
 1 ..TCCGTTATCG GGCCTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA  
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGCTTgGG  
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAG ACTTGTTCC GCCGCAAGAA  
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC  
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA  
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT  
 301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA  
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTCG CGAAGCCAAT GCCGAAGCCA  
 401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC  
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA  
 501 AGAAAGCAAT ACGCTGATTA TGCCGCCCAA TGTTGCCGAC ATCGGCAGCC  
 551 TGATTCTGCG CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)  
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE  
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA  
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV  
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng)

from *N. gonorrhoeae*:

m519/g519

				10	20	30
m519.pep				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
		40	50	60	70	80
m519.pep		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
		150	160	170	180	190
		100	110	120	130	140
m519.pep		IQQSEGEAQAQAVNASNAEKIARINRAKGEAESLRLVAEANA AEAIRQIAAALQTQGGADAV				
g519		IQQSEGEAQAQAVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV				
		210	220	230	240	250
		160	170	180	190	200
m519.pep		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAEQYVTAFAKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq  
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA  
 51 ATCCTTTGTT GTCATCCAC ACAGGAAGT CCACGTTGTC GAAAGGCTCG  
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT  
 151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTAGACGT

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201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGGCCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATT CCGCCGCCCT TCAAACCCAA GCGGTTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFQFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GOREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDG SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
a519 YFQVTDPKLSYGSNNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GANGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||
a519 GANGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
|||||
a519 IQQSEGEAQAANASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
|||||
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCGCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CTTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGT AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCG CCGCATCAAC CGGCCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATT CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

```

g519-1.pap

1	MEFFIIILLAA	VAVFGFKSFV	VIPQQEVHVV	ERLGRFHRAL	TAGLNILIPF
51	IDRVAYRSLA	KEIPLDVPSQ	VCITRDMTQL	TVDGIYIFQV	TDPKLSAYGS
101	SNYIMAITQL	AQTTLRISVG	RMELDKTFEE	RDEINSTVVS	ALKEIAGAW
151	VKVLRYEIKD	LVPQQEILRA	MQAQITAEER	KRARAASEGR	RDIAEQINLAS
201	GQREAEIQQS	EGEAQAAVNA	SNAEKIARIN	RAKGEAESLR	LVAAENAEAI
251	RQIAAALQTS	GGADAVNLKI	AEQYVAAFNN	LAKESNTLLM	PANVADIGSL
301	SAGMKKIIDS	SKTAK*			

m519-1.seq

1	ATGGAATTTT	TCATTATCTT	GTTGGTAGCC	GTGCGCGTTT	TGGGTTTCAA
51	ATFCCTTTGTT	GTCATCCCAAC	AACAGGAAAT	CCACGTTGTC	GAAGAGCGTGG
101	GGCGTTTCCA	TGCGCGCGTG	ACGCGCGGTT	TGAATTTATTT	GATTCCTCTTT
151	ATCGACCCGCG	TGCGCTACCG	CCATTGCTGT	AAAGAAATCC	CTTTAGACGT
201	ACCCAGCCAG	GTTCTGCATCA	CGCGCGACAA	TAGCAGAGTC	ACTGTTTGACG
251	GCATCATCTA	TTTCCAAGTA	ACCGACCCCA	AACTCGCCTC	ATACGGTGTG
301	AGCAACTACA	TTATGGCGAT	TACCCAGCTT	GCCCAAAACGA	CGCTGCGTTC
351	CGTTATCGGG	CGTATGGAGT	TGGACAACAA	GTTTGAAGAA	CGCGACGAAA
401	TCAACAGTAC	TGTTTGTGCG	GCTTTGGAGC	AGGCGCGCGG	GGCTTGGGGT
451	TGAAGGTTT	TGCGTTATGA	GATTAAAGAC	TGGGTTCCGC	CCGAGAAGAT
501	CCTTCGCTCA	ATGACGGGCG	AAATTACTGC	CGAACGCGAA	AAACGCGCCC
551	GTCATCGCGA	ATCCGAAGGT	CGTAAATTCG	AACAAATCAA	CCTTGCCGAT
601	GGTCAGCGCG	AAGCCGAATC	CCAACAATCC	GAAGGCGGAG	CTCAGGCTGC
651	GGTCAATGCG	TCAAATGCGC	AGAAAATCCG	CCGCATCAAC	CGCGCCCAAT
701	GTTGAAGCGA	ATCCTTGCCG	CTTGGTTGCC	AAGCCAAATC	CGAAGCCCAT
751	CGTCAAATTC	CGCGCGCGCT	TCAAACCCAA	GCGGGTGCGG	ATGCGGTCAA
801	TCTGAAGATT	CGGGAACAAT	ACGTGCTGTC	GTCAACAAT	CTTGCCAAAG
851	AAAGCACTGC	GCTGATTATG	CCGCGCAATG	TGCGGCAATC	CGGAGCGCTG
901	ATTTCGTCCG	GATAGAAAT	TTCCGACAGC	AGCAAAAACG	CCAAATATA

m519-1.

1	MEFFIILLVA	VAVFGKFSV	VIPQQEVHV	ERLGRFHRAL	TAGLNILIPF
51	IDRWYRHTSL	KEIPLDVPQS	VCITRDNTQL	TVDGIIYFQV	TDPKLASVGS
101	SNYIMATLQL	AQTTLLRSVIG	RMELDKTFEE	RDEINSTEVA	ALDEAAGAW
151	VKVLRYEIKD	LVPPQEIILRS	MQAQITAEER	KRAINAESEG	RKIEQINLAS
201	GQREAEIQQS	EGEAAQAVNA	SNAEKIARIN	RARGEAESLR	LVAEANAEAI
251	RQIAAALQQT	GGADAVNLKI	AEQYVAAFNN	LAKESNTLIM	PANVADIGSL
301	ISAGMKIIDS	SKTAK*			

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFFIILAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSLS					
m519-1	MEFFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSLS					
	10	20	30	40	50	60
	70	80	90	100	110	120
g519-1.pep	KEIPLDVPSPQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTILRSVIG					
m519-1	KEIPLDVPSPQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTILRSVIG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMAQAQITAERE					
	130	140	150	160	170	180
	190	200	210	220	230	240
g519-1.pep	KRRIAEESEGRKIEQINLASGQREAEIQQSEGEAQAAVNNAEKIARINRAKGEAESLR					

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTGTG GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCGA GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCATTATGA GATTAAAGAC TTGGTCCGCG CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AATTACTGCG TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAATCAA CCTTGCCAGT
601 GGTGAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCC AGAAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATT CCGCCGCCCT TCAAACCAA GCGCGTGGCG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51 IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQITLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESG RKIEQINLAS
201 GQREAEIQQS EGEAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQKSFVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFGKSFVVIQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQITLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQITLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKK
              |||||
m519-1      ISAGMKIIDSSKTAKK
              310

```

### Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt ttgttttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgcccga caattcgacc aagacatcga cgtctttacg
351 cgcgaaacagt tcgaacggat cttttgacaa gggcggggcg cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa ataccgattt
451 cgcgccccc aa gggcggggaa atttcctctg cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCACT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTTCGGrK AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GCGGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

```



301	GCAATGCCGG	TACCGCCGaA	CAATTCGACG	ACGACATCGA	CGTCTTCACG
351	TGCGACCAGT	TCGAACGGAT	CTTTGACAAA	GGCTGc.CGG	ACGGGCAGGT
401	TTGTCCGGCT	TTTTCTTCAC	TCAAATCGCA	CACGGCAGAA	ATACGGATTT
451	CGCGCCCCAA	GCGACGGGAA	ATTTCTCTCG	CGTGTCTsCG	CAACACGGCA
501	GCGCTACCGC	CGCCAGCCGT	ACCCAAACCT	AAAAAGACGA	TGTTTACTGG
551	CTTCATTGTG	TCTCCTTGTA	AGCCGACTGA	AATGTAAATA	TTGA

m520.pcp

```

1  MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILFAA KPSRRALMIG
51 IPPATAASNW TMTFCFSASG KISLPYSASS FLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTROQYGF
151 RAPSDGKFPP RCXATROPYR RRPYPNLKDR CLLASCLLV SRLKCKY*

```

### Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m520/g520

		10	20	30	40	50	60
m520.pep		MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNW					
		:					
g520		MPALLSIRANALPFSRISERMKLLVPLIMPAMDLILFAAKPSRTALMIGIPPATAASNW					
		10	20	30	40	50	60
		70	80	90	100	110	120
m520.pep		TMTFCFSASGKISLPYSASSFLLAVTMCLPFMSAFNTASLAMPVPPNNSTTTSTSSRATS					
							:
g520		TMTFCFSASGKISLPYSASSFLLAVTMCLPFMSAFNTASLAMPVPPNNSTKTSTSLRANS					
		70	80	90	100	110	120
		130	140	150	160	170	180
m520.pep		SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
		:	:	:			:
g520		SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR					
		130	140	150	160	170	180
		190					
m520.pep		CLLASLCLLVSRLLKCKY					
g520		CLLASLCLLVSRLLKCKY					
		190					

a520.seq

1	ATGCCTGCGC	TTCTTTCACT	ACATCGG.CA	AACGCGCTGC	CTTTTTCGCG
51	CATTTTCGGAG	AGGATGAAGT	TGCTGGTGCC	GTTAATAATG	CCGGCGATGG
101	ATTTAATCCT	GTTTGCCGCC	AAACCTTCGC	GCAGGGCTTT	GATGATTGGG
151	ATACCGCCCG	CTACTGCCGC	TTCAAATTGG	ACGATGACGT	TTTGTTTTTT
201	CGCCAGCGGG	AAGATTTTCT	TGCCGTATTC	GGCGAGCAGT	TTTCTTTGGT
251	CGGTAAACGAT	GTGTTTCCGC	TTTCCAATGG	CTTCAACAC	CGCATCTTTG
301	GCAATGCCGG	TACCGCCGAA	CAATTCGACG	ACGACATCGA	CGTCTTCACG
351	TGCGACCAGT	TCGAACGGAT	CTTTGACAAA	GGCTG.CGG	ACGGGCAGGT
401	TTGTCCGGCT	TTTTCTTCAC	TCAAATCGCA	CACGGCAGAA	ATACGGATT
451	CGCGCCCCAA	GCGACGGGAA	ATTTCTCTCG	CGTTGTCCCG	CAACACGGCA
501	GGCGTACCAG	GCGCGACCGT	ACCCAAACCT	AAAGACCGA	TGTTTACTGG
551	CTTCATTGTG	TCTCCTTGTA	AGCCGACTGA	AATGTAATA	TGTA

a520.pep

```

1  MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRRALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLAVTMCLP F5MAFN7ASL
101 AMPVPNNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

783

151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY\*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNATSLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNATSLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCCGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTGGCA ATGCCCGTGC
251 CGCGGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCCGCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGCTCTC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1466; ORF 520-1.ng&gt;:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNATSLA MPVPPNNSTT TSTSLRATSS
101 NGLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCCGTTG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTTCACTAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCCGCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGCTCTC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1468; ORF 520-1&gt;:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNATSLA MPVPPNNSTT TSTSSRATSS

```

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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
151 TVPKPKRPMF TGFIVSPCKP TEM\*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
	10	20	30	40	50	60
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
g520-1.pep	SHMAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
m520-1	SHTAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT  
51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA  
101 CTGCCGCTTC AATTGGACG ATGACGTTT GTTTTCCGC CAGCGGGAAG  
151 ATTTGCTTGC CGTATTCGGC GAGCAGTTT TTGTTGGCGG TAACGATGTG  
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC  
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTCG  
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC  
351 TTCACCTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC  
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGCAGCCGT ACCGCCGCCG  
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC  
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK  
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS  
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
151 TVPKPKRPMF TGFIVSPCKP TEM\*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTFCFSASGK	ISLPYSASSF	
	10	20	30	40	50	60
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
a520-1.pep	SHMAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
m520-1	SHTAEIRISRPK	RREISSALSRNT	AAVPPPTVPK	PKRPMFTGFIV	SPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

1 ATGAAATCAA AACTCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG  
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG  
101 AAACCGTTTA CACCACCAAG CCGTCTAAA GCTGCCACTC AACCGATTG

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```

151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

g521n.pep

```

1 MKSKLPLILI NLSLISSPLG ANAAKIYCT INGETVYTTK PSKSCHSTD
51 PPIGNYSSER YILPQTPEPA PPSNNGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDROQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

m521.seq

```

1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAsCAAG CCGTCCAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTGTG AAATATAAAG
251 CCCCAGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521.pep

```

1 MKSKLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
51 PPIGNYSSER YIPPQTPEPV SSPNNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/g521

	10	20	30	40	50	60
m521.pep	MKSKLLILINFLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
	:       :       :       :       :       :					
g521	MKSKLPLILINLSLISSPLGANAAKIYCTINGETVYTTKPSKSCHSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
	:       :       :       :       :       :       :					
g521	YILPQTPEPAPSPNNGQAVKYKAPVKTVSKPAKSNTPP-QQAPVNNRRSILEAELSNE					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	:       :       :       :       :       :					
g521	RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLDROQNIQALQRELGRMX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

a521.seq

```

1 ATGAAATCAA AACTCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

```

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```

51  CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAA GCTGCCTCTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAGAGA
501 ATTGGGACGT ATGTAA

```

-- This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSLSTDL
51  PPIGNYSSER YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQQN IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAXIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
a521	MKSKLPLILINFSLISSPLGANAAXIYTCTINGETVYTTKPSKSLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRRSILETELSNE					
	:       :					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDQRQQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDQRQQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtgtgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgct gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtg
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcggtt ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
51  KPQAKQKIVE SCMNIPFAE KWQNDLKARG LDADNTRLAV DYCKMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```

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301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC  
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG  
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS  
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKMWEQP  
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGKLGAQEQ					
	:             :       :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKMWEQPLDGLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	:             :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG  
 51 CAAAAAAGCA AAAGCCAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA  
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCAATG CGCGATGTCC  
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCCTGA AGAATATTCC  
 201 GTTTGCCGAA AAATGGCAAA ACGATTGCG GGCCCGCGGT TTAGATTCAA  
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT  
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC  
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG  
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS  
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKMWEQP  
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE\*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGKLGAQEQ					
	:					
a522	SCVKNIPFAEKWQNDLRARGLDSDNNTRLTVDYCKMWEQPLDRLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120

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```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51 gacgggaacg gtttatcttt tggttgtcag cgcggtttg gcgggttcgg
101 gcattgccta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcaactgctt ccgcgctggg catttggttc gtacatgcc aaccgccgt
201 gggaaaagt gaaacggatt catatcagga ttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt ttttatcgc
301 ggtacgcact ggcaggcgca aaatacggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcacgtcc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAL AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  .GCCGCTCTAA TCATCGAATT ATTGACGCGA ACGGTTTATC TTTGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCAT TGCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  .AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDL AGQYVEILRH TGNRYEVFY RGTWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSALAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSALAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|||||:|

```

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g523 LIVRKEGNLLIIANPX  
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
1  ATGACTGTAT GGTGTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51  GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CCGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
1  atgaagtacg tccggttatt ttctctcggc acggcactcg ccggcactca
51  agcggcggtc gccgaaatgg ttcaaatcga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcctgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 gccgaattga aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaaagca ccgcccgaac tactgggggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 LQLKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:



```
m525.pep
1  MKYVRLFXLG AAIAXTOXAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGRSRYPFKA
101 GELKQPVTNV SWXAAAYCA QAGKRLPTID EWEFAGLASA TQKXRLKRTR
151 LOPHYSLRVC RRRTERPARC RXKAARTTGA FMICTG*
```

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m525.pep		MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLK KDTGLIKVKPFKLDKYPVTNAEF					
			:				
g525		MKYVRLFFLTALAGTQAAAAEMVQIEGGSYRPLYLK KDTGLIKVKPFKLDKYPVTNAEF					
		10	20	30	40	50	60
		70	80	90	100	110	120
m525.pep		AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTVNSWXAAANAYCA					
						:	
g525		AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTVTNISWFAANAYCA					
		70	80	90	100	110	120
		130	140	150	160	170	180
m525.pep		AQGKRLPTIDEWEFAGLASATQKXRLKRTLQPHYSRLVCRRRTERPARCRXKAARTTGA					
						:	
g525		AQGKRLPTIDEWEFAGLASATQKXRLKRTLQPHYSRLVCRRRTERPARCQSTARTTGV					
		130	140	150	160	170	180
m525.pep	FMICTGX						
g525	FMICTGX						

```

a525.seq
1  ATGAAGTTTA CCCGGTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCCGCCCG
101 TTATCTGAAA AAAAGATACG GGCCTGATTa AAGTCAAACC GTTCAAAC TG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCGCAATT TG CCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGCCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGCATTTAA AACAAACCGT AACCAATGTT TCCTGGTTTC CCGCAAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTTGAC GAATGGGAAT
401 TTGCCGGA CTGCTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACCCG CATTATCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGACACGATG CTGCAAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLLEFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

	10	20	30	40	50	60
m525.pep	MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
a525	MKFTRLLEFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525.pep	AEFVNSHPQWQKGRIGSKQAEPAAYLKHHMKNGSRSYAPKAGELKQPVNTVSWXAANAYCA					
a525	AEFVNSHPQWQKGRIGSKQAEPAAYLKHHMKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525.pep	AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRTTERPARCRRXKAARTTGA					
a525	AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCQXVARTTGA					
	130	140	150	160	170	180
m525.pep	FMICTGX					
a525	FMICTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCCGC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAGAGACC GCCGAACTA CTGGGGTGT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKDRPNYWG VYDMHGLIEWE TEDFNSLLS
201 SGNANAQMEF SGASVGASDS SNYAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

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```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGGCAATTAA AACCAACCGT AACCAATGTT TCCTGGTTTG CCGCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1  MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVNTV SWFAANAYCA AQKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG VYDMHGLIEW TEDFNSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLFGRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL DKYPVTNAEF					
g525-1	MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL DKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVNTV SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVNTI SWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQKRLPTIDE WEFAGLASAT QKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
g525-1	AQKRLPTIDE WEFAGLASAT QKNGSNEPG YNRTILDWYADGGKRLHDV GKDRPNYWG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWE TEDFNSLLS SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV					
g525-1	YDMHGLIEWE TEDFNSLLS SGNANAQMFC SGASVGSADS SNYAAFLRYG IRTSLQSKYV					
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLFGRCTSRX					
g525-1	LHNLFGRCTSRX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1  ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCGCG
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGGCAATTAA AACCAACCGT AACCAATGTT TCCTGGTTTG CCGCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

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This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGRKDLHDV GKGRPNYWG VYDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

      10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVNTAEF
      |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a525-1      MKFTRLFLC AALAGTQAAA AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVNTAEF
      10      20      30      40      50      60

      70      80      90     100     110     120
m525-1.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVNTVSWFAANAYCA
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a525-1      AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA
      70      80      90     100     110     120

      130     140     150     160     170     180
m525-1.pep  AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGKRLHDVGKGRPNYWG V
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a525-1      AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWG V
      130     140     150     160     170     180

      190     200     210     220     230     240
m525-1.pep  YDMHGLIEWE TEDFNSSLLSSGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a525-1      YDMHGLIEWE TEDFNSSLLSSGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV
      190     200     210     220     230     240

      250
m525-1.pep  LHNLGFRCTSRX
      |||:|||||
a525-1      LHNLGFRCTSRX
      250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atgggttttac cagtctcctt ttttcagcct gtccagttgg cggcggtcgc
51  gcttggtcgg tctgccgtcg ggatgggcgg aagtgatgcg gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtctctctc
151 atacagaagc cgcgcctcgg gtgccgggcg gcggttggtg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggtttact gtttttgact ttcgagccgt ttacttgaac
301 cctaccagct tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcgggaaga atcgtgcttg
401 tctttcatac gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLVPSFFQP VQLAAVALGR SAVGMGGS DA AELVELFALF PQCCRFRVFF
51  IQKRLGCRA ALVVQTFNLD FMKGIERQV DNIADVYGT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTTCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCYTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

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201 TAACCKTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGty GrTwATaTCG  
 251 CsGATGTmTA TGGTTTTACT GTTTTtGACC TCGAGCCGT TTACTTGAAC  
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC  
 351 GTGCCGCCCA AAGCCATTtG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG  
 401 TCTTTCATAC GATTTTGTtT GAAATAATTG AATTTGTtTC GAGTTTAGCA  
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep

1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRVRVLF  
 51 IQKPRXGCRA ALVVQTFNtD FIGKXNXASV XXIADVtGFT VFDLRAVYLtN  
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA  
 151 \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRVRVLF	IQKPRXGCRA
g527	MVLPSVFFQP	VQLAAVALGR	SAVGMGGSDA	AELVELFALF	PQCCRFRVFFI	QKPRLGCR
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNtD	FIGKXNXASV	XXIADVtGFT	VFDLRAVYLtN	PTQFDVLLRK	GTGLEKTCRP
g527	ALVVQTFNtD	FMGKIERQVD	NIADVtGFT	VFDRAVYLtN	PTQFDMLLRK	GTGLEKTCRP
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
g527	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq

1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCCG  
 51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG  
 101 TCGAGCTGTT TGCCTCTTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC  
 151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT  
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG  
 251 CCGATGTCTA TGGTTTTACT GTTTTtGACC TTCGAGCCGT TTACTTGAAC  
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC  
 351 GTGCCGCCCA AAGCCATTtG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG  
 401 TCTTTCATAC GATTTTGTtT GAAATAATTG AATTTGTtTC GAGTTTAGCA  
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep

1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLF  
 51 IQKPRLGCRAL ALVVQTFNtD FIGKGIERQV DNIADVtGFT VFDLRAVYLtN  
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA  
 151 \*

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRVRVLF	IQKPRXGCRA
a527	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRFRVLF	IQKPRLGCR
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNXXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
			:			
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggtaataaa atatacgga acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 ccggtctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcggcgaga gtccgctgtc ttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatcct
251 acttttatag gaaaataggg aagtttgaag cctgcgggtt ggattggcgt
301 acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctggttgtaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLVER FKQGGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTTACA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLVERFKQGGFDCLE					
	70	80	90	100	110	120

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```

m528.pep      K
               |
g528          KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDG NR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFACGLDWRTRDGKPLIETFKQEGFDCLK					
	70	80	90	100	110	120

```

m528.pep      K
               |
a528          KQGLRRNGLSERVRWX
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1  ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCTTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPLSLED YEIPLSDG NR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```

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```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

```

m528-1.pep..
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAIDFWDI
51  GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRV KYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPLSLED
          |||:|||| |||:||||||| |||:||||||| |||:||||||| |||:||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
g528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||:||||||| |||:||||||| |||:||||||| |||:||||||| |||:||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||:|||||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

```

a528-1.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

```

a528-1.pep
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPPSLED
          |||:||||||| |||:||||||| |||:||||||| |||:||||||| |||:||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90      100     110     120
a528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
          |||:||||||| |||:||||||| |||:||||||| |||:||||||| |||:||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90      100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||:|||||||
m528-1      KQGLRRNGLSERVRWX
          130

```



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

g529.seq (partial)

```

1 atgacccata tcaaaccctg cattgccgcg ctgcactca tcgggcttgc
51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggctgcaccg cctgatcaaa ctggaagtcc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc ggctcggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgct cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgcgt tgacggcaaa tcccccgccg aaatctccgc
351 cgctttctg.

```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

g529.pep (partial)

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

m529.seq

```

1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGTCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTG CGGCAAGTCT CTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 TACTCCACC GCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAAGC AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCCT CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCTTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

m529.pep

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAEVLKSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPALQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGKDKDQTV WQSPSPDPNL EAAFLTRFMQ YLGVDDQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

          10      20      30      40      50      60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA

```

799

```

m529      |||||
          MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
          10      20      30      40      50      60

          70      80      90      100     110     120
g529.pep  GSGAVRAGDLEKRRTPAVQQPADAGSIEKRQRRPLRAATAANAWLVVDGKSPAIESAAFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m529      GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLER-DGSQRWLVDGKSPAIEWPLLK
          70      80      90      100     110

m529      AFWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVR
          120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1523>:

```

a529.seq
1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTCGAAGTCC CACCTGATT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTGCG CGGCAAGTCT CATGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGCGCCG CCTATTCGAC ACAGTCGGTT TGGGCGGCAT
501 CTAATCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTACC GAACAAAAC CCGCCTGTG
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTGCCA ACGGCTCGCG CATCGCTCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAACTC CATTCCGAAC TGC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1524; ORF 529.a>:

```

a529.pep
1  MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
51  DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAEVLKSV KGVRLERDGS
101 QRWLVDGKS HAEIWPILLKA FWQENGFDIK SEEPaIGOME TEWAENRAKI
151 PQDSLRLRFD TVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDITV WQSPSPDENL EAAFLTRFMQ YLGVDDQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRALAL DRIGLTVVGQ NTERHAFVQ
301 KAPNESNAVT EQKPGLEKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*

```

m529/a529 99.2% identity in 375 aa overlap

```

          10      20      30      40      50      60
m529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
          |||||
a529      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPDQGNLYRLPA
          10      20      30      40      50      60

          70      80      90      100     110     120
m529.pep  GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSPAIEWPLLK
          |||||
a529      GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSHAIEWPLLK
          70      80      90      100     110     120

          130     140     150     160     170     180

```

800

```

m529.pep  FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDKVLGGIYSTGERDKFIVRI
           |||||
a529       FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDTVLGGIYSTGERDKFIVRI
           130      140      150      160      170      180

           190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQSPSPDNLEAFLTRFMQYLGVDGQQAEE
           |||||
a529       EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQSPSPDNLEAFLTRFMQYLGVDGQQAEE
           190      200      210      220      230      240

           250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFVLQ
           |||||
a529       NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFVLQ
           250      260      270      280      290      300

           310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPLFKRLLGKGKAEKPAEQPELIVYAEFPVANGSRIVLLNKDGSAYAG
           |||||
a529       KAPNESNAVTEQKPLFKRLLGKGKAEKPAEQPELIVYAEFPVANGSRIVLLNKDGSAYAG
           310      320      330      340      350      360

           370
m529.pep  KDASALLGKLHSELRX
           |||||
a529       KDASALLGKLHSELRX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga gcgcggaat gacgggttg atatgggtca tctgtcatc
51  ctgtgtgatg gatattaaag tgtttgcgat gttatgccgt ccgaacggtt
101 cagacggcat ggctatatatt aaagtgtgcc tgaggcttcc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtcgcg atccgcccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVLRLSGRR
51  GLLXVRLPSA ERAAGGRAVR IPRRIPPIS VRRDWVRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  WTGAGTGCGA GCGCGGCAAT GACGGGTYTG ATATGGGTCA TCGTGTCATC
51  STGTGTGATG GATATTAAAG TGTYTGTTGC GWTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTIONTGC WTGTCCGTTT YCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TCGGGTTCGC ATCTGCCCAg GCGGATACC GCCCATTTTC GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVLRLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep  XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVLRLSGRRGLLXVRFPSA 60
           |||||

```

g530	MSASAAMTGLIWWIVSSCVMDIKVFVMLCRPNNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRI <del>C</del> PGRI <del>P</del> PISVRRGWVRRTWCRKSESVGR	99
	:            :       :	
g530	ERAAGARAVRIRPRRI <del>P</del> PISVRRDWRRTWCRKSESAGR	99

```
a530.seq
1      ATGAGTGC GA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTATC
51     CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101    CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGCGGCGCG
151    GGACTTTTTC CTGTCCGCCT TCCGTACAGC GAACAGCGCG CAGGCGGAGC
201    TCTCGGTTGC ATCTGCCGAC GCGGATACCC GCCCATTTCC GTGCGGCGGG
251    GTCGGGTTTC GACAACATGG TGTCTAAAT CGGAATCAGC CGTGCTGTGA
```

a530.pep  
1 MSASAAMTGL IWVIVSSCVI DIKVFVALCR PNGSDGMAIF KVLRLSGRR  
51 GLLPVRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR\*

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA					
a530	MSASAAMTGLIWVIVSSCVMDIKVFALCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA					
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRI PCGRIPPI SVRRGWVRRTWCRKSES VGRX					
a530	ERAAGGRAVRI PCGRIPPI SVRRGWVRRTWCRKSES AGRX					
	70	80	90	100		

```
g531.seq
  1  ATGACCGCCC  TACTCGTCAT  CCTCGCCCTC  GCCCTGATAG  CCGTCGGCAC
51  GGCAGGCATC  GTCTATCCCG  CCCTGCCCGG  CTTGGCATTG  ATGTTTGCCG
101 GAACATGGCT  GCTTGCCTAT  GCCGCGCGCT  ATCAAATCTA  CGGCGCAGGC
151 ATCTTGTGGA  CGGTCGGACT  CATCAGCCTT  GGCGGCATAC  TGGCGGACTA
201 TATGGCAGCG  ATGTTGGGGG  TAAAATACAC  TGGGGCAGGC  AAACTCGCCG
251 TCCGAGGTGC  ATTGGCCGGC  AGCATCATCG  GCATATTTT  CTCCTTCCC
301 GACTAATAC  TCGGCCCTT  TATCGGCGCG  GCGCGAGCG  AACTGATCGA
351 TCGGCGCAAT  ATGCTTCAG  CAGGTAAGC  GGGCTTGGT  ACGCTGTTGG
401 GCGTTGCTGT  CGGCACGGCG  TTCAAATCG  GCTGCGCGGT  ATCCATCTTG
451 TTTATCTGT  TGGTGAATA  CATCGCATA  CTGTTTTAA
```

```
g531.pep
  1  MTALLVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
51  ILWTVGLISL GGILADYMAG MLGVKYTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIDRRN MLQAGKAGLG TLLGLVVGTG FKIGCAVSIL
151 FILLVKYIAY L
```

```
m531.seq
1 ATGACCGTCAT TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51 GGCGGGCATC GTTTaCCCCG CCCTCGCCGT ATTGGCATTG ATGTTTGGCG
101 GAACATGCGT GCTTGGCTAT CGCGCGCGCT ACCAAATCTA CGCGCGCGGC
151 GTTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGCATAC TGGCGGACTA
201 TGTGGCAGGC ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
251 TTCGCGGCGC ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
301 GGACATATAC TCGGTCCCTT TATCGCGCGC CGCGCAGGCG AACTGATCGA
```

m531.pap

1 MTVLTVILAL ALIavgTAGI VYPALPLAL MFAGTWLLAY AGGYQIYGAG  
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLAVRGALAG SIIGIFFSLP  
101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL  
151 FILLVKYIAY LF\*

Homology with a predicted ORF from *N. gonorrhoeae*

m531/q531

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1535>:

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTTGCT	GCTCGCCTAC	TCCGCGCGCT	ACCAAATCTA	CGCGCGGGGC
151	GTTTTGTGGA	CGGTGGGACT	CATCAGCCTT	GCCGGCATAC	TGGCGGACTA
201	TGTGGCAGGC	ATGTGGGGGA	CAAAATATAC	CGAGCAGGCG	AAGCTCGCCG
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	GCGCAGGCG	AACTGATCGA
351	ACGGTCAATC	ATGCTTCAGG	CAGGTAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTACTCG	CGGTACGGCG	TTCAAAATCG	GCTGCGCCGT	ATCCACTCTG
451	TTTATCTCTG	TGGTGAATAA	CATCGCCTAC	CTGTTTTAA	

This corresponds to the amino acid sequence <SEQ ID 1536; ORF 531.a>:

a531.pcp

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG  
51 VLWTVGLISL AGILADYVAG IWGTYKTGAG KLAVRGALAG SIIGIFFSLP  
101 GLILPFIGA AAGELIERN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL  
151 FILLVKYIAY LF\*

m531/a531 96.9% identity in 162 aa overlap

	10	20	30	40	50	60
m531.pep	MTVLTVILALIALI	AVGTAGI	VYPALPGLAL	MFAGTWLLAY	AGGYQIYGAG	VLWTVGLISL
	:					
a531	MTALLVILALIALI	AAGTAGI	VYPALPGLAL	MFAGTWLLAY	SGGYQIYGAG	VLWTVGLISL
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGI	WGTKYT	GAGKLAVR	GALAGSII	GIFFLPGLIL	GPFGIAAAGELI
						ERRN

803

```

|||||
a531      AGILADYVAGIWGTYKTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERRN
              70      80      90      100      110      120

              130      140      150      160
m531.pep  MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
|||||
a531      MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
              130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cccccgcgt gatttgtggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgctgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgt
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDCA
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GCGCGCGCTG AATTGCCGCT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CCGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GCGCGGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACCGGTC GCGGCGTGGT CGTGATGCTC ATTTGGTTGA GTTTGTTACA
501 CGTCGGCATT ACCGATTTCG GCGGCGGCTT CCGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCGCGTACCG
751 TTTAAATACG GTTTTGCTTT CCACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTTGGCTGA CCGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTTCCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTG GTCAGTCACG GCATCCGCAG GCGCGAAGCG
1201 GTGATTCGCG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVVL IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

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201 VLVFNCKMNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLFPV  
 251 FKYGFADFWDH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL  
 301 RGGLVADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL  
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA  
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT  
 451 EAAVKFDDH LEH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLS IQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLS IQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT CTCGTTTCGT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT TTCGGCGTGG CTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGTGACA
501 CGTCGGTATT ACCGATTTTCG GCGCGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCCGA TGAGCGGCAT
651 TGCGGTTCGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCACGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATATG GTTTTGCTTT TGAATGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTG ACGGCGACGG
851 CAATGGTGTC CGACGACCGG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGCGGCGG TGTGGCGGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTGCACA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCT CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACCTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGCG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

```

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```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSEFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAGV LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFADFWDH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

## m532/a532 100.0% identity in 463 aa overlap

```

      10      20      30      40      50      60
m532.pep MSGQLGKGADAPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532      MSGQLGKGADAPDLVYGLEDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
      10      20      30      40      50      60

      70      80      90     100     110     120
m532.pep AYLVSAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
a532      AYLVSAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
      70      80      90     100     110     120

      130     140     150     160     170     180
m532.pep ISTLLGVSEFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
a532      ISTLLGVSEFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
      130     140     150     160     170     180

      190     200     210     220     230     240
m532.pep ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAGVLIAGYIVALFLGKVDFSALQ
a532      ADGTFGSMENLGLASLVLLIVLVFNCMKNP LLRMSGIAGVLIAGYIVALFLGKVDFSALQ
      190     200     210     220     230     240

      250     260     270     280     290     300
m532.pep NLPLVTLVPVPFKYGFADFWDHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
a532      NLPLVTLVPVPFKYGFADFWDHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
      250     260     270     280     290     300

      310     320     330     340     350     360
m532.pep RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG
a532      RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG
      310     320     330     340     350     360

      370     380     390     400     410     420
m532.pep RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAIAAATSVGLGLGVAFEPEVF
a532      RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAIAAATSVGLGLGVAFEPEVF
      370     380     390     400     410     420

      430     440     450     460
m532.pep KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
a532      KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
      430     440     450     460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1   atgccctttc ccgttttcag acaantattt gcttngtcc tgcacggtt
51  ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatctaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttcgccc tgtttgaagt

```



```

g535.pep
1  MPFPVFRQXF  AXSLLRFFAV  GRILESDISN  SGFSETINAS  NVFFVGYEYP
51 ACISNLHRFQ  FKLGIQFFH  ALFAEVDGQS  GGFAFVCGID  NHAGAEGFVT
101 DVLSDAEACV  GLRLFEVIDD  FVPLYGGLAR  VAVAVEGGFF  DQGVVQYFWR
151 DFDEAGCDA  ELGLSVQHAL  LCHGDVEAFA  GAGDGDVHEA  AFFFEAAALG
201 KAHFAGETPL  FHTGEEDGVE  FQAFGGVDGH  QLDGFFACPC  LVFAGFEGGV
251 AOEGDEGGG  IV*

```

```
m535.seq
1  aTGCCTTtC CCGTTTTcAG ACgGCCTTTT GCTTTGTCCT TACTtACGTT
51  TTTTGCCGTA AGTCAGATTc TTGTATCCGA CATTtCCAAc ACgCGGTgTT
101 CGGAACAcaT AGACgCGTcA AATgTtTTTg TCGGATAcGA ATATCCgACC
151 TAcATTTCaA ATTTAcATcT CTtCCAATTg CGCAAAcTTg GTGTCCAaCT
201 CTTTcACGcC CTgTTTGCCg AAATTgATgG TcAGTCGGGc GgATTcCGcCT
251 TTATcTGCgG CATcGATAAT CACGCCgGTg CCGAATTgG CGTGGcGGAc
301 GTTTTGTCCg ATAcGGAAAc CTGCgTAGGT TTGGGcGTGT TGTAGTcGT
351 cGATGATTTT ATcTTTGGAT GCGcCGGTtT GGCcGTGTt GCCGTAAcTG
401 TCGTAGGcAG GcTTTTTGAc GGCAGGTAG TGCaATAcTt CGGTGGGATt
451 CTCTTCGAcG AAGCGGGAGa CGATGCCGAa TTGGGTtTGT cGTGCAGAcA
501 TGCGTGTGTG CGCCATGGTG ATGTAGAGGc GTTgCGGGc GCGGGTGATG
551 GCGAcGTAcA TGAGGCGGCG TtCTtCTTCg AGGCCGCCGc GTTCGGCAAG
601 GcTCATTTCg CTGGGGAAGc GGCCTtCTTC cATGCCGTG AGGAAGAcGG
651 CGTTAAATTC CAAGcCTTTg GCGGCGTGGA CGGTcATGAG TTGGAcCGGC
701 TTTTCGCCTG CGcTCGCCTG GtTTTCACCG GATTCAGGGc CGGCATTGCT
751 TAGGAAGGGc AGAATGGGGA AGGCCGGGTc GTCTGA
```

```
m535.pep
  1  MPFPVFRPPF  ALSLLTFFAV  SQILVSDISN  SGVSETIDAS  NVFVGYEYPT
  51  YISNLHLFQF  RKLGVQLFHA  LFAEIDGQSG  GFAFICGIDN  HAGAEGFVAD
101  VLSDTETCVG  LGLFVVVDDF  IFGCGGLARV  AVTVVGRLFD  GQVVQYFGWD
151  LFDEAGDDAE  LGLSVQHALL  RHGDVEAFAG  AGDGDVHEAA  FFEFAAAF GK
201  AHFAGAAAF  HAGEEDGVKF  QAFGGVDGHE  LDGLFACACL  VFTGFEGGIA
251  XEGENEGGV  V*
```

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	59
m535.pep	MPFPVFRRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEPTYISNLHLFQ					
	:            :              :            :					
g535	MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ					
	10	20	30	40	50	60
	60	70	80	90	100	119
m535.pep	FRKLGVLGFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDD					
	:  :      :      :      :      :      :      :      :					
g535	FRKLGIQFFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLEFVIDD					
	70	80	90	100	110	120

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	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRLLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	:      :    :        :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	

	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	:     :     : : : : : : : : : : : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVFQAFGGVDGHLQDGLFACPC						
	190	200	210	220	230	240	

	240	250	260
m535.pep	LVFTGFEGGIAXEGENEGGGVV		
	:    :     :    :		
g535	LVFAGFEGGVAQEGEDGEGGIV		
	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq (partial)

```

1   TTCAGACGGC CTTTTCCTT GTCCTTGCTA CAGTTTTTTG CCATAGGTGC
51  GATTCTCGAA TCCGACATTT CCAACAGCGG TTTTTCGGAA ACGATAGACG
101 CGTCAAATAT TTTTGTGCGA TACGAGTATC CAGCCTGCAT TTCAAATTTA
151 CATCGCTTCC AATTTCGCAA ACTTGGTGTC CAACTCTTTC ACGCCCTGTT
201 TGCCGAAATT GATGGTCAGT CGGGCGGATT CGCCTTTATC TGCGGCATCG
251 ATAATCACGC CGGTGCCGAA TTTGGCGTGG CGGACGTTT GTCCGATACG
301 GAAACCTGCG TAGGTTTGGG GCTGTTGTA GTCGTCGATG ATTTTGTCTT
351 TGGGCGCGGC GGTTCGCGC GTGTTGCCAT AGCGGTCGTA GGCGGGTTT
401 TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTTCTT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTGTCCGTG CAGCATGCGT TGTGCGCCA
501 TGGTGATGTA GAGGCGTTG CGGGCGCGGG TGATGGCGAC GTACATCAGG
551 CGGCGTTCTT CTTCGAGGCC GCCGCGTTCG GCAAGGCTCA TTTGCTGGG
601 GAAGCGGCCT TCTTCCATGC CGGTGAGGAA TACGGCGTTA AATCCAAGC
651 CTTTGGCGGC GTGCACGGTC ATGAGTTGTA CGGCTTTTTC GCCGCGCCT
701 GCTTGGTTT CGCCGATTTC GAGAGCAGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGCGG GGGTCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

```

1   FRFPFALSLL QFFAIGRILE SDISNSGFSE TIDASNIFVG YEYPACISNL
51  HRFQFRKLG VQLFHALFAEI DGQSGGFAFI CGIDNHAGAE FGVADVLSDT
101 ETCVGLGLF VVDVDFVGRG GLARVAIAV GGFDFGQVVQ YFGRDFFDEA
151 GDDAELGLSV QHALLRHGDV EAFAGAGDGD VHQAFFFEA AAFGKAHFAG
201 EAAFFHAGEE YGVKFQAFGG VGHELYGFF ARACLVFAGF ESSIA*ESD
251 GEGGVV*

```

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGYEYPTYISNLHLFQF					
	:             :     :					
a535	FRFPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGYEYPACISNLHRFQF					
	10	20	30	40	50	

	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110

	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRLLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	:       :      :        :					
a535	VFGRGGLARVAIAVVGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

```

          190      200      210      220      230      240
m535.pep  AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKQFAFGGVDGHELDGLFACACL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
a535      AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKQFAFGGVHGHelyGFFARACL
          180      190      200      210      220      230

          250      260
m535.pep  VFTGFEGGIAXEGENGEGGVVX
          ||:||||:||||:|||||
a535      VFAGFESSIAXESEDGEGGVVX
          240      250

```

q537.seq

1	atgaaatccc	tttttatttg	gtcgtctcta	ttgggctcgg	cggcaggcgt
51	tttctaccat	acccaaaacc	aatccctgcc	cgcgggcgaa	cttgtctatc
101	cgtccgcacc	gcaaatcagg	gacggcgggc	atgcgctgca	ctaccccaac
151	cgcattccga	cacaaatcgg	tttgcacgcg	ctggcacacg	cgcggctttt
201	ggaaaattcc	cgcgcagcgg	acgcacgcgt	tctcacgctc	aatcccggaag
251	acggacacgg	gccacaccaat	cccgacaatc	cgcactacac	cgcacaaaag
301	ctgaccgaac	gcacacgcct	tgccgggtat	ctctacaacg	gcgtgcatga
351	aaacatcagc	acggaagagg	aagccgcgga	atcgtccgac	agcgacatcc
401	gcacgcagca	acgccaagtg	gacgctttga	tgagcgcaat	ctaccacgcg
451	ctttcgtgtc	ttgaccgcga	taccgacgaa	gcaggtgcgg	ctatttgttcg
501	cgaaaaccggc	aaaaccgtcc	tcgtattcaa	tcaggggcaac	ggcagcttcg
551	agcgcgcctg	tgcaaaagga	aggcggcagc	cggaaagcagg	acggaaatat
601	taccgcaacg	cttgccacaa	cggtcgggcc	gtttatgctg	acgaagccat
651	gcccgtaaag	gaattgtctt	ataccgccta	tcgggttggc	ggcggtcgcc
701	tgccttattt	ttacggggaa	cgctcccgac	ccgtgcttgcg	atattgaatc
751	acaggcaatc	ctgcgcagcat	tgatttttcc	gaggcggcag	gcaaaattgc
801	gatgaaaagt	ttcaagctgt	atcagggtaa	aaacgaaatc	cgccccgtca
851	gggttttaac	cgcgcggcaac	gaccctaacg	gcaggctgac	cgcgcaccaaa
901	ttcgcccttt	tcccgctcaa	acctttggaa	tacggcacgc	tttatacggc
951	ggtatccgac	tatgtccgca	acggacggca	cgcgcaggcg	aaatggcaat
1001	ttagaaccgg	aaaaccggat	taccttatt	ttagggtaaa	cggcggcgag
1051	acacttgctg	ttagaaaaagg	cgaaaaatat	ttcatccact	ggcgcggagc
1101	ctggtgtctg	gaagcgtgta	cccgttatac	ctaccggcgg	cagttcgcca
1151	acagcctgtc	catactccgg	cacgaagcgg	gcggcattgt	cttcagcgtc
1201	agcggaatgg	cgggaagcgc	catcaggctt	acctcggaag	acagcccgga
1251	acqcqgtgta	accttttatt	tgcaggattg	a	

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MSLFIWLL  LGSAGVFYH  TQNQSLPAGE  LVYSPAPQIR  DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEVAEESD  SDIRTQQRQV DALMSAYIYHR
151 LSLLDRLHTE AGAAVFRENG KTVLVFNQGN KSFERACAKG RROQEAGRYK
201 YRNACHANGAA VYADEAMPVT ELLYTAVPVG GGALPYFYGE RPDVPPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPRVRLTAGN DPNGRLTAHQ
301 FALFPLKPLE YGTLRYAVFD YVRNGRHAQA KWQFPTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIIHWTRGVFL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERG  TLYLOD  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

1	ATGAAATCCC	TTTTTATTCG	GCTGCTCCTG	TTGGGTTCCG	CGGCAGGCGT
51	TTTCTACCAT	ACCCAAAmCC	AATCCCTGCC	CGCGGGCGAA	CTTGTCTATC
101	CGTCCGACC	GCAAATCAGG	GACGCGGCGC	ATGCGCTGCA	CTACCTCAAC
151	CGCATCCGAG	CCCAATTCGG	TTTGCACAAG	CTGGCACACG	CGCCCGTTTT
201	GGAAACTCC	GCCCGCagGC	ACGCAAGCTA	CCTCACGCTC	AATCCCGAAG
251	ACGGCACAAG	CGAACAACAT	CCCGACAATC	CGCACTACAC	CGCACAAAAA

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301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)  
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN  
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK  
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR  
 151 LSLDRHTDE SGAA...

-- Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng)

from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIR DGGDALHYLN RIRAQIGLHK					
	:					
g537	MKSLFIWLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIR DGGDALHYLN RIRTAQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
	:					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN					
	130	140	150	160	170	180
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq  
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT  
 51 TTTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC  
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC  
 151 CGCATCCGCG CCCAAATCGG TTGACACAAG CTGGCACACG CGCCGGTTT  
 201 GGAAATTC GCGCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG  
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG  
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG  
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG  
 551 AGCGGCATTG CGCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT  
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT  
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC  
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC  
 751 ACGGGCAATC CTGCCAGCAT TGATTTTCC GAGGCGGCG GCAAAATTAC  
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGTCA  
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA  
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC  
 951 GGTATTTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT  
 1001 TTAGAACCGG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG  
 1051 ACACCTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG  
 1101 CTGGTGTTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

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```

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTCAGCGTT
1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGAAG GAGAAACGGA
1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

```

a537.pep
  1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPPEYEI
251 TGNPASIDFS EAAGKITMKS FKLQYQKNEI RPYRVLTAGN DPNGRLTAYQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RFGSRLSISR HKAGGIVFSV
401 DGMAGSRITL APEGETERGV TLYLQD*

```

m537/a537 98.2% identity in 164 aa overlap

```

              10      20      30      40      50      60
m537.pep    MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNLRIRAQIGLHK
              |||||
a537         MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNLRIRAQIGLHK
              10      20      30      40      50      60

              70      80      90      100     110     120
m537.pep    LAHAPVLENSARRHASLYTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              |||||
a537         LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              70      80      90      100     110     120

              130     140     150     160
m537.pep    TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDESGAA
              |||||
a537         TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDEAGAAFVRENGKTVLVFNQGN
              130     140     150     160     170     180

a537         GRFERHCAQGRNQPEAGRKYRYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE
              190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

```

g538.seq
  1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51 cgtcatgctg gtggcgctaa tgttgataa agatgatacg ggcagcaatg
101 ccgccctgct gaacggtttt cagacggcat tggcggaagc cgtcagactg
151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaacgcga
201 ccgccgcac actgcgtgtt ttgtcggcac gggcaaggcg gcggagctgt
251 cggaagcagt tgccgcagac ggcattgatt tggctgtatt caaccacgaa
301 cttactccca cgcaggaacg caatttgaa aaaatcctcc aatgcccgct
351 attggacaga gtgggctga ttctggcgat ttctgccgcg cgcgcccgca
401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
551 ccgcccatcg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
601 cagcgcgccc tgcgccgcaa gtcccgcgag tcgggcagaa tcaaaacggt
651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatcctgac
801 cgataccgct ggattcgtca gcgatctgcc gcacaaactg atttccgcct
851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgct
901 gtcgatgctg ccgcccgga cagcgggcag cagattgaag acgtggaaaa
951 cgtactgcaa gaaatccatg cccacgatat tccgtgcacg aaggtgtaca
1001 acaaaaaccga cctgctgccc tctgaagaac aaaacacggg catatggcgc
1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaaatac

```

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

```

g538.pep
  1  MSGRTGRNSA  TQAQPERVML  VGVMLDKDDT  GSNAARLNGF  QTALAEAVEL
 51  VKAAGGDSVR  VETAKRDRPH  TALFVGTGKA  AELSEAVAAD  GIDLTVFNHE
101  LTPTQERNLE  KILQCRVLDL  RGLILAI FAR  RARTQEGRLQ  VELAQLSHLA
151  GRLIRGYGHL  QSQRGGIGMK  GPGETKLETD  RRLTAHRINA  LKKQLANLKK
201  QRALRRKSRE  SGRIKTFALV  GYTNVGKSSL  FNRLTKSGIY  AKDQLFATLD
251  TTARRLYISP  ACSIIILDTV  GFVSDLPKHL  ISAFSATLEE  TVQADVLLHV
301  VDAAARNSGO  QIEDVENVLQ  EIHADHIPC I  KVVNKTDLLP  SEEQNTGIWR
351  DAAGKIAAVR  ISVAENTGID  ALREAIAEYC  AAPNTDETE  MP*

```

-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

```

m538.seq
  1  ATGACAGGCA  GAACAGGCGG  CAACGGCAGT  ACCCAAGCGC  AACC CGAACG
 51  CGTCATGCTG  GTGGGCGTAA  TGTGGACAA  AGATGGTACG  GGCAGTAGTG
101  CCGCCCGTCT  GAACGGT TTT  CAGACGGCAT  TGGCGGAAGC  TGTCGAGCTG
151  GTCAAAGCGG  CGGGCGGCGA  TTCCGTGCGC  GTGGAGACTG  CCAAACGCGA
201  CCGTCCGCAC  ACCGCGCTGT  TTGTCGGCAC  GGGCAAGGCG  GCGGAGCTGT
251  CAGAAGCAGT  TGCCGCGAGC  GGCATCGATT  TGGTCGTATT  CAACCACGAA
301  CTCACGCCCA  CGCAGGAACG  CAACCTTGAA  AAAGAACTsA  AATGCCGCGT
351  ATTGGACAGG  GTAGGGCTGA  TTCTGGCGAT  TTTCGCTCGC  CGCGCCCGCA
401  CGCAGGAAGG  CAGGCTGCAA  GTCGAGTTGG  CGCAATTGAG  CCATTTGGCG
451  GGACGCTTGA  TACGCGGTTA  CGGCCATCTG  CAGAGCCAGC  GCGGCGGTAT
501  CGGCATGAAA  GGCCCGGCG  AAACCAAAC  GAAAACCGAC  CGCCGATTGA
551  TCGCCCATCG  GATCAATGCC  TTGATAAAC  AGCTTGCCAA  CCTCAAAAAA
601  CAGCGCGCCC  TCGCGCGCAA  GTCnCGCGAA  TCGGGCACAA  TCAAAACGTT
651  TCGCTGGTGC  GGCTATACAA  ATGTCGGA  ATCCAGCCTG  TTCAACCGGC
701  TGACAAAGTC  GGGCATATAT  GCAAAGGACA  AGCTTAGTCC  CGAATGCAGC
751  ATTATCCTGA  CCGATACCGT  CGGATTCGTn  AGCGATCTGC  CGCacAAACT
801  GATTTCCGCC  TTTTCGCC.A  CGCTGGAAGA  AACC GCGCAA  GCCGATGTGC
851  TGCTGCACGT  CGTCGATGCC  GCCGCTCCGA  ACAGCGGACA  GCAGATTGAA
901  GACGTGGA  ACGTACTGCA  AGAAATCCAT  GCCGCGGATA  TTCCGTGCAT
951  CAAGGTGTAC  AACAAAACCG  ACCTGCTGCC  GTCTGAAGAA  CAAAACACGG
1001  GCATATGGCG  CGACGCTGCG  GAAAAATTG  CCGCCGTCCG  CATTTCGGTT
1051  GCTGAAAATA  CCGGTATAGA  CGCACTGCGC  GAAGCcATTG  CCGAGTCTTG
1101  TGCCGCCGCA  CCAAACACAG  ACGAAACCGA  AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

```

m538.pep
  1  MTGRTGGNGS  TQAQPERVML  VGVMLDKDGT  GSSAARLNGF  QTALAEAVEL
 51  VKAAGGDSVR  VETAKRDRPH  TALFVGTGKA  AELSEAVAAD  GIDLTVFNHE
101  LTPTQERNLE  KELKCRVLDL  RGLILAI FAR  RARTQEGRLQ  VELAQLSHLA
151  GRLIRGYGHL  QSQRGGIGMK  GPGETKLETD  RRLIAHRINA  LIKQLANLKK
201  QRALRRKSRE  SGTIKTFALV  GYTNVGKSSL  FNRLTKSGIY  AKDKLSPECS
251  IILDTVGFV  SDLPHKLISA  FSXTLEETAQ  ADVLLHV VDA  AAPNSGQQIE
301  DVENVLQEIH  AGDIPCIKVY  NKTDLLPSEE  QNTGIWRDAA  GKIAAVRISV
351  AENTGIDALR  EAIAESCAAA  PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	:      :                   :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLTVFNHELTPTQERNLEKELKCRVLDL					
	:					
g538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLTVFNHELTPTQERNLEKILQCRVLDL					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI	FARRARTQ	EGRLQVELA	QLSHLAGRL	IRGYGHLQ	SQRGGIGMKGPGETKLETD
g538	VGLILAI	FARRARTQ	EGRLQVELA	QLSHLAGRL	IRGYGHLQ	SQRGGIGMKGPGETKLETD
	190	200	210	220	230	240
m538.pep	RRLIAHR	INALIKQL	ANLKKQ	RALRRKS	RESGTIKT	FALVGYTNVGKSSLFNRLTKSGIY
g538	RRLTAHR	INALIKQL	ANLKKQ	RALRRKS	RESGRIKT	FALVGYTNVGKSSLFNRLTKSGIY
	250	260	270	280		
m538.pep	AKDKL-----	SPECSIIL	TDTVGFV	SDLPKLI	SAFSXTLE	ETAQADVLLHV
g538	AKDQLFATL	DDTTARR	LYISPAC	SIILTD	TVGFVSD	LPKLI
	290	300	310	320	330	340
m538.pep	VDAAAPNS	GQQIED	VENVLQ	EIHAGDI	PCIKVYN	KTDLLPSEEQNTGIWRDAAGKIAAVR
g538	VDAAARN	SGQQIED	VENVLQ	EIHAGDI	PCIKVYN	KTDLLPSEEQNTGIWRDAAGKIAAVR
	350	360	370	380		
m538.pep	ISVAENT	GIDALRE	AIAESCA	AAAPNTD	ETEMPX	
g538	ISVAENT	GIDALRE	AIAEYCA	AAAPNTD	ETEMPX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1   ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCG TTCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTCGCCCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCGCGCAA GTCCCGCGAA TCGGGCACA TCAAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAACTG ATTTCGCTC
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAATA
951 CGTACTGCAA GAAATCCATG CCGCGCATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGCA CCTGCTGCGG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1   MTGRTGRNGS TQQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVALD GIDLVVFNHE
101 LTPTQERNLE KILQCRVLDL VGLILAI FAR RTAQEGRQL VELAQLSHLA
151 RLIRGYGHL QSRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

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201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD  
 251 TTARRLYISP ECSIILDTV GFVSDLPKLI ISAFSATLEE TAQADVLLHV  
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR  
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP\*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRV LDR					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRV LDR					
	70	80	90	100	110	120
m538.pep	VGLILAI FARRARTQEGRLQVELAQ LSHLAGRLIRGYGHLQSQ RGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQ LSHLAGRLIRGYGHLQSQ RGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538.pep	RRLIAHRINALIKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALKKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538.pep	AKDKL-----SPEC SIILDTVGFVSDLPKLI SAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISPEC SIILDTVGFVSDLPKLI SAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
m538.pep	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538.pep	ISVAENTGIDALREAIAESCA AAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCA AAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagtgcc ggcaacggca
101 aggcggacga tgtattgttt gcgttccttt tggttgccgg cttcgatttt
151 ttgcgcgtca tagggtgcgg cgggttagcc tgtctgccgg attttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt ccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggattgg
401 acttcgggca ggtcgtacag gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt tttttcgcgt cggcgggtgc tcgtttgtaa taactgcca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggt ctttcgcctt gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtgga aacagggttt tttcatggca tttcgggttc

```



```

651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgctcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatategttg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgtt gttccggcgg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgacagg tttcttccaa
951 ggtggcgga aagggcgaaa tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgccgtcg tgctcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccggttga acaggttga tttgccgaca ttggtatag

```

-- This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

```

g539.pep
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QGFFFRVGGG SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPLFRA
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

```

m539.seq (partial)
1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCGTCGT CCCAGACGAC GCGGCaGcGg
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCAGC CTCGCGCGTG CCGCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTGCG TCGAGGATTT CTGGGGCGG
451 CAGCTCGGTT TTTTGCCTG CCGCGGTGCG TTGTTGTAA TAAGTCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaGcGg
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACA GTCAGGTGGA GGTGTTCCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGACGCGT CGCGCCATAT GCCCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTC TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTGTCAGTAC GTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGCG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CThACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

```

m539.pep (partial)
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLFRVGGG LFVITAQARV NNALCDRLTA GAQGFVAVVF VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

```

m539/g539
10      20      30      40      50      60
m539.pep MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
|||||
g539 MEDLQEIGFDVAAVKVGRQREHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

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	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFVAVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFVAVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539.pep	130	140	150	160	170	180
	LARAAGVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGVGFHKVGLDFGQVVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539.pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFVGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSFTSTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSFTSTSSICCPFLFA					
	250	260	270	280	290	300
m539.pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVSVRAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTCTTT TGGTTGGCGG CTTGATTTT
151 TTGCGCGTCA TAGGGTGC GGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCTGTACG GCGGATTGG TCGAGGATT CTTGGGGCGG
451 CAGCTCGGTT TTTTGGCGGT CCGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GCGCAGCAG
551 GTTTCGCGGT CTCGTTTTC GTAACGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGA AACAGTTTT TTTTATGGCA TTTGCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGAGCGT CGCGCCATAT GCCCGTGTTT TGTCTTTAG ACGGCAGCAG
801 GTCGGTTTGT TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCAGCG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CCGCGCGTCG TGTCGAGTGT GCGGAAAAGC TGGTCTTTCG CATATATGCC
1101 CCACTTGGTC AGCCGGTTGA ACAGACTGGA TTGCGGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHRRLHHPQP GNGEADDVLF AFFLVGGFDF

```

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51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK  
 101 LLFDQPDAGG AGDAAEH\*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR  
 151 QLGLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVFVE VTDGQMVFVG  
 201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF  
 251 PAASRHPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA  
 301 AASTTCSSTS ACAVSSVAE KAEISLCGRS LTNPTVSVRI MLHSGLMYSR  
 351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV\*

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQ	IGFDVAAVKVGRQREHRLHHPQPGNGEADDV	LF	FAFFLVGGFDFLRVIGCGGVA		
a539	MEDLQ	IGFDVAAVKVGRQREHRLHHPQPGNGEADDV	LF	FAFFLVGGFDFLRVIGCGGVA		
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
a539	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDRLTA					
a539	LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDCLTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
a539	GAAGFAVAVFVFTDGQMVFVGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPLFGA					
a539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPLFGA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
a539	AASTTCSSTSACAVSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGMLYSRRRAVVSSVAKS					
	310	320	330	340	350	360
a539	WSFAYMPDLVSRLNRLDLPTLVX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

1 atgccgccct cccgacgcgg caacgggggtg ttttatcaaa acggcaaact  
 51 tgccaatgcg gtttcgctt gccgattgcc aaaccggcaa acctttcccg  
 101 tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcggtgtg  
 151 ttatttgctc actcggacgg gtgcaggttc gtattgtgtc gattcgtcgc  
 201 cgtaatacag cagcgcgagt ttgacgggga tgcgtccctg cgatttgccg  
 251 tgggcggttg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg  
 301 gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgcccgcgc  
 351 ctttcgcgca gttgaagtcc caataggcca catcatcgta aggcgcggcg  
 401 gcacggtgtc cgcagtcgtt gatttgccc atatttttcc agcgtga

This corresponds to the amino acid sequence &lt;SEQ ID 1568; ORF 540.ng&gt;:

g540.pep

1 MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

```
m540.seq (partial)
1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTGTG
51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCTCTG TGGTAGAAGT
201 TTTTCAGCTTT GCTGATTTCG ATCATGCGCG CGCTGCGGCC GCCTTTTGCGC
251 CAGTTGAAAT CCCAATACAC ACATCATCGT TAAGGCGCGG CGGCGCGGTG
301 TCCGCAGTCG TTGATTTCG CCAATATTTT CCAGCGTGA
```

```
m540.pep      (partial)
1      ..PNPMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
51      GIPQGIGTTA IFLLEVETFE ADFNHARAAA AFAPVEIPIH HIIVRGGAV
101     SAVVDLRHIF PA*
```

m540/g540

```

m540.pep      10      20      30
                PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                |||||
g540      GNGVIFYQNGKLANAVSACRLPNRQTFVPVPVNPMPSEPSDGIGCLFVHSDGCRFVLCRFV
                10      20      30      40      50      60

                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFVAVGIGIPQGIGITTAIFLLVEVFTFADFNHARAAAAAFAPVEIPIH
                |||||::|||:| |||::|:|||||:|||||:|||||:|:|
g540      AVIQHAEFDGDASLRFAVGVGIAQGIRAAAVFLLVEVFADFNFHTRAAAAAFAPVEVPIG
                70      80      90      100     110     120

                100     110
m540.pep      HIIVRRGGAVSAVVDLRHIFPAX
                |||||:|||||
g540      HIIVRRGGTVSAVVDLRHIFPAX
                130     140

```

```
a540.seq
  1  ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAA ACGGCAAAC
51  TGCCATATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTTCCCG
101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTCAGACGG CATCGGGTGT
151 TTATTGTGCC ACCCGGATGG GTGCAGGTTG GTATTGTGTC GATTCGTGTC
201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTTGCGG
251 TGGGGCTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCTGCTG
301 GTAGAAGTTT TCACGTTTGC TGATTTCAAT CATACGCGCG CGGCCGCGC
351 CTTTGCGCCA GTTGAATACC CAATACACCA CATCATCGTA AGCGCGGGC
401 GCGCGCGCGC CGCAGTCGTT AATCTGGTTC ATGTTTTCC A
```

a540.pep (partial)

```
1  MPSSRRNGV FYQNGKLANA VSDCLPNRQ TFPVMPNPM PSEPSDGIGC
51  LFVHPDGCRF VLCRFVAVIQ HAEFDGDSAL *FAVGVGIPQ GIGTTAIFLL
101 VFTTFADFN HTRAAAAFAP VEIPIHHIIV RRGGAAAAVV NLVHVFP
```

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m540/a540 92.8% identity in 111 aa overlap

		10	20	30
m540.pep		PNMPSEPSDGIGCLFVHPDGGRFVLCRFV		
a540	GNGVFYQNGKLANAVSDCRLPNRQTFVPMPNPNMPSEPSDGIGCLFVHPDGGRFVLCRFV			
	10 20 30 40 50 60			
		40	50	60
m540.pep	AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHARAAAFAFVEIPIH			
a540	AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHTRAAAFAFVEIPIH			
	70 80 90 100 110 120			
		100	110	
m540.pep	HIIVRRGGAVSAVVDLRHIFPAX			
a540	HIIVRRGGAAAAVNLVHVFP			
	130 140			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

g542.seq  
 1 atgccgaaat ggtcgcgcat acggcggttg agcgctcttt cgctgatgtt  
 51 cagcgcggt gtcagccggt tgacttggtg tgcgccgccg tcgaacgcgg  
 101 cattcaggtt gcggtggaag tcttcagacg gcatagcgtc tgcttccgcc  
 151 gtttgccccg ccgcccggctc gatgccgtct gaaaccgtgt cccacaaatc  
 201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatggt tcgcccaaat  
 251 gcccctttgg gacgggttgc aggcaggatg ccgccaagcc gcgcaggttt  
 301 gggggcaaat cccatatact gaccggttcg cggtaa

This corresponds to the amino acid sequence &lt;SEQ ID 1574; ORF 542.ng&gt;:

g542.pep  
 1 MPKWSRIRRC SVLSLMFSAA VSRLTWCAFP SNAEFRVRLK SSDGIASASA  
 51 VCFAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF  
 101 GGKSHILTGS R\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

m542.seq  
 1 ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT  
 51 CAGCGCGTCT GTCAGCCGCT TGACTTGGTG TGCGCCGTCG GCAAACGCGG  
 101 CATTTAGGTT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC  
 151 GTTTGCCCGG CCGCCGCGCC GATGCCGTCT GAAACCGTGT CCCACAAGTC  
 201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT  
 251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC  
 301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1576; ORF 542&gt;:

m542.pep  
 1 MPKWSRIRRC SVLSLMFSAS VSRLTWCAFP ANAEFRVRLK SSDGIASASA  
 51 VCFAAGSMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF  
 101 RQDAAKPRRF GGKSHILTGS R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

m542/g542

	10	20	30	40	50	60
m542.pep	MPKWSRIRRC SVLSLMFSAS VSRLTWCAFP SNAEFRVRLK SSDGIASASAVCPAAGPMPS					
g542	MPKWSRIRRC SVLSLMFSAA VSRLTWCAFP SNAEFRVRLK SSDGIASASAVCPAAGSMPS					
	10	20	30	40	50	60
		70	80	90	100	110
m542.pep	ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF GGKSHILTGS RX					

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```

|||||
g542      ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100      110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT GGTCCGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGA CTTGATG TGC GCCGCCG GCAAACGCGG
101 CATT CAGGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GSKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
              |||||:|||||
a542           MPKWSRIRRC SVLSLMFSVSASRLTXCAPPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              |||||:|||||
a542           ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atgggtttgtc ggattatttgc cgccgttttt ggctttcaac tcggcaatca
51  gcccgtcgat gccttttggt ttgatgattt cgccgaattg gttgcggtac
101 acggttaacca ggctcgtgcc ttcgatggcg acgttgtagg tacggtattt
151 gccgcccgtt tggtaggtgg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgctt
351 gtttttgcgc gtcggacgcg gtacgccaag ggttgccgac cgccaatgcg
401 gtcatacgtt ggaaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggtcaaa acctgtgtgg
501 cgttttgccg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgtcta aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcctgaaaa tggatgtgta tgtttattct gcgctttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcagg tttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccggcagca aggttttccg tatcgccgcc ctgctgcagc ccgatgtact
801 gttcgcctaa aagtcccga gtcaggattt gcgcggaaac gtcactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctcgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggtt
951 tgacgggggc attgacctt aaaccgccga tgcgcgcaa atcggcataa
1001 acggcgtaag ttttgtccga accgcggaac gccgcgccc ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgccgcgcc gatcaagacg aacagtccga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF GFQLGNQPV DAFGDDFAEL VAVHGNQARA FDGDVVGTVF

```

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51 AAALVGKGVH IDGLLTGDAD FGTDDDFLAA LIDDGIVFDV DGRVFEFQHR  
 101 AGIGADQQGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW  
 151 ACRSRVAAFE DGQNLGCVLA DLSHCVRGG KCHADAQNTD AQCADEGGFF  
 201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQN HCRTGYGDGV  
 251 AGSKVFRIAA LLQPDVLFQA KRSQDLRGN VTAEILILAVQ IKAHPRLIGF  
 301 RVKPSADAP DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA  
 351 ESEKGNRRRA DQDEQSDPKF QYVLFH\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

m543.seq  
 1 ATGGTTTGTG GGTATTGTC CGCCGTTTTT GGCTTTCAAC TCGGCAATCA  
 51 GTCCGTCCAC GCCTTTCGCT TTGATAATT CGCCGAATTG GTTGC GTAC  
 101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATT  
 151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTGCCCGG  
 201 GTACGCCGAC TTCGCGCGCG ACGATGATT CTTGCCGCC TTTATTGACG  
 251 ATGGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT  
 301 GCCGAATAG GTGCGGATCA GCAGGTTTG AAATCTTTG GCCAACGCTT  
 351 GTTTTTCGCG GTCCGACGCG GTGCGCCAAG GGTGCCGAC CGCCAATGCG  
 401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTGT  
 451 GCGAGCGGTG TTGCGATCGC CGTTTTTAA GATGCTCAAT ACTTGAGTGG  
 501 CGTTTTGACG GATTGGCTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG  
 551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGG AGGATTTTTT  
 601 CATGATTAAG TGTCTAGT TGAATATGAT GCATACGTT TATTCGCGCG  
 651 CTTTTCCGC ATTGCCGCG TCGGCATTTT TCTCGGCAA ACTCGTCATG  
 701 AATTGCGCGA TAAGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT  
 751 GGTGTCGCGC GCAGCAAGGT TTTCCGTGTC GCGCCCTGC TGCAGCCCGA  
 801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG  
 851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA  
 901 GGATTTGCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCTG  
 951 CGGATTGAC GGGGCGATTG ACCTCAAAC CGCCGATGTC GCCGAAATCG  
 1001 GCATAACCG CGTAAGTTTT GTCCGAACCG CCGAACGCC CACCGCCGGC  
 1051 CACGCGGAAA GCGAGAAAG CAACCGCCG CGCGCCAATC AGGACGAACA  
 1101 GTCCGACCA AAATCCAAT ATGTTCTTCT TCATTAA

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

m543.pep  
 1 MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF  
 51 TAALVGGEVH VDGFLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFQHR  
 101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL  
 151 ASGVGIAVFX DAQYLSGVLT DLAYRVGRGG KCHADAQNTD AQCADEGGFF  
 201 HDXVSXFEYD GIRLFGGFFR IAAVGIFLKG TRHEFADKVF QNHCRGYGD  
 251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI  
 301 GFRVKSADSAD APDQYACGFD GGIDLQADV AEINGVSF VRTAERRTAG  
 351 HAESEKGNRR RANQDEQSDP KFQYVLLH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng)

from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVF	GFQLGNQSVH	AFRFDNFAEL	VAVHGNQARA	FDGDVVGTVF	TAAALVGGEVH
g543	MVCRLFAAVF	GFQLGNQSVH	AFRFDNFAEL	VAVHGNQARA	FDGDVVGTVF	TAAALVGGEVH
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYAD	FGADDDFFAA	FIDDGIVFDV	DVGVFQHR	RAGIGADQQGL	KFFGQRLFLR
g543	IDGLLTGDAD	FGTDDDFLAA	LIDDGIVFDV	DGRVFEFQHR	RAGIGADQQGL	KFFGQRLFLR
	70	80	90	100	110	120
	130	140	150	160	170	180

```

m543 . pep      VGRGAPRVADRQC GHTLEIEIGNRIGFGFVWAGVIAVFXDAQYLSGVLTDLAYRVGRGG
|||:||||||||||||||||||| | :|| :| |||:|:: ||||
g543            VGRGTPRVADRQC GHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLCGVLADLSHCVGRGG
              130          140          150          160          170          180

              190          200          210          220          230          239
m543 . pep      KCHADAQNTDAQCADEGGFFHDXVSKFEYDG-IRLFGGFFRIA AVGIFLGKTRHEFADKV
||||||||||||||||||| | :| :| |||||||::: ||:: ||:|:|
g543            KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
              190          200          210          220          230

240          250          260          270          280          290          299
m543 . pep      FQNHCRCTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAEELILAVQIEAHPRL
|||||||||||||||||||:|||||||||:|||||||||:|||||||||:||||
g543            FQNHCRCTGYGDGVAGSKVFRIAALLQPDVLFQAQKSRSDLRGNVTAEELILAVQIKAHPRRL
              240          250          260          270          280          290

300          310          320          330          340          350          359
m543 . pep      IGFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
|||||||||||||||||||||||||||||||||||||||:|||||||||
g543            IGFRVKPDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRAARHAESEKGNR
              300          310          320          330          340          350

360          370          379
m543 . pep      RRANQDEQSDPKFQYVLLHX
|||:|||||||||||:|
g543            RRADQDEQSDPKFQYVLFHX
              360          370

```

a543 seq

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLAAVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGVEV VDGFLPGXAD FGADDDDFFAA FIDDXIVFDV DGVVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGRNRIGEGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLEGGFFR IAAVGIFLGK TRHEFADKVF QNHCRGTGYD
251 VGASKSVFRV AALLQPDVLL AQKRSQDLR GNVAAELILA VQIEAHPRLI
301 GFRVKSDDFA APDQYACGFD GGIDLOTADV AEIGINGVSF VRTEARRTAG

```



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351 HAEEKGNRR RANQDEQSDP KFQYVLFH\*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
a543	MAYGLLAAVXSLQLXNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIIDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
a543	VDGFLPGXADFGADDDFFAAFIIDDXIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGI FLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGI FLGKTRHEFADKVF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCRTRYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAELILAVQIEAHPRLI					
a543	QNHCRTRYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAELILAVQIEAHPRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQTDADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQTDADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgcgcgc gactgatcg gcatcctcct
51  cgccaccgct ctcaccccg acagtaaaac cgcgcccgcc ttctccctgc
101 cgcacctgca cggaaaaacc gtttccaacg ccgacctgca aggcaaagtc
151 accctgatta atttttggtt tccctcctgt ccgggttggt tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgtc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcgaaac cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence &lt;SEQ ID 1586; ORF 544.ng&gt;:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

1	ATGAwAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCGG	ACAGCAAAC	CGCGCCCGCC	TTCTCmTGC
101	CCGACCTGCA	CGGAwAAAAAC	GTTTCCAACG	CCGACCTGCA	AGGCAAGTAT
151	ACCCGTGATTA	ATTTTTCGGT	TCCCTCCTGT	CCGGGTGTGTG	TGAGCGAwAT
201	GCCCAAAATC	ATTAwAACGG	CAATGACTA	TAAAwCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGACAAAGC
351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCTTATCG
401	GCAAAATAAGG	CGAAATCTTC	AAAACCTACG	TCGGCGAACC	CGATTTCCGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	CGCGAATAG	

m544.pcp

```

1  MXKILTAADV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIQK*GEIF KTYVGEPDFG
151 KLYOEIDTRV AQ*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m544/q544

	10	20	30	40	50	60
m544.pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGVTLINFWFPSC					
	:					
g544	MKKILTAAAVALIGILLATVLIIPDSKTAPAFSLPDLHGKTVSNADLQGVTLINFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	:               :					
g544	PGCVSEMPKVTKTANDYKKNDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
	:					
g544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

a544.seq

1	ATGAAAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCCG	ACAGCAA AAC	CGGCCCCGCT	TTCCTCCGTG
101	CCGANCTGCA	CGGAAAAANC	GTTTNC AACG	CCGAGCTTGA	AGGCNAAGTT
151	ANCCTGATTA	ANTTTTGGTT	TCCCTCCTGT	CCGGGTTGTG	TGAGCGCAAT
201	GNCANAAATC	ATTA AAACGG	CAATGACTA	TAAAAACA AA	TAATTC CAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTTCGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAAAAGG	CGAAATCCTC	AAA ACTTATG	TCGGCGTACC	CGATTTCCGG
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

a544.pcp

1 MKKILTAADV ALIGILLAIV LIPDSKTAPA FSLXLHGKX VKNADLQGXV  
51 XLIXFWFPSC PGCVMEXXI IKTANDYKNK NFQVLAQAQ IDPIESVRQY  
101 VKDYGLPFTV MYDADKAVGO AFGTOVYPTS VLGKKGEIL KTYVGEPEFG

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151 KLYQEIDTAL AQ\*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTA	AAVVALIGILLAIVL	XPDSKTAPAFSXPDLHGKTVSNADLQ	QKVTLINFWFPSC		
a544	MXKILTA	AAVVALIGILLAIVL	IPDSKTAPAFSLSLXHLGKXVXNADLQ	GXVXLIXFWFPSC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
a544	PGCVSEMXXIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
a544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq  
 1 atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgcccacaaat  
 51 cgtcgaaact ttcgacgtat tcttctttag gaacgattgc gccttttttta  
 101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggg atatctcggt  
 151 gatataattta caagatgacgg cttcgagatt ccgaaccgct cctttaaaga  
 201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg  
 251 ccgaagtcga gatggatgcc cattacttcc cttactcag aaaatatatta  
 301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg  
 351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaacggaa  
 401 aaaagcgggt tgttttttgt tgtaa

This corresponds to the amino acid sequence &lt;SEQ ID 1592; ORF 547.ng&gt;:

g547.pep  
 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV  
 51 DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL  
 101 KFIMLHIVTN IRVFCVCVKE LLTILVKNL PNGKKRFVFC C\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq  
 1 ATGTCGCTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT  
 51 CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTTTA  
 101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT  
 151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCT CTTTAAAGA  
 201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG  
 251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA  
 301 AAATTATATA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT  
 351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTTG TCTCCAAACG  
 401 GAAAAAAGCG GTTGTGTTT TGTGTGTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1594; ORF 547&gt;:

m547.pep  
 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV  
 51 DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL  
 101 KFIMLHIFTN IKVFXVCVK ELLTILVKNL SPNGKKRFV CC\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng)  
 from *N. gonorrhoeae*:

m547/g547

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	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
g547	ELLTILVKNLSPNGKKRFVFCCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```

a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAACG  GTAGCGAGTT  TTGCCCAAT
51  CGTCGAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTSTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTTACATAT  ATTTACAAAT  ATTAAAGTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T

```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```

a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLKYL
101 KFIMLHIFTN  IKVFXCVCVK  ELLTILV

```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```

g548.seq
1  atgttttccg  taccgcgttc  ctttttgccg  ggcgttttcg  tacttgccgc
51  gcttgccgcc  tgcaaacctc  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgcggct  gcggaata  cggcaagcc  gcaaacgcgc
151 ggtacggata  tgcgtaagga  agacatcgcc  ggcgatttca  cactgaccga
201 cggcgaagcc  aagcctttca  gcctgagcga  ttgaaagcc  aaggtcgtga
251 ttctgtcttt  cggccttacg  cactgtcccg  atgtctgccc  gacagggctt

```

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```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acggggcgccc aaaacctgcc ggtcatcaag cagcaatacc gcgtgggttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtgc gtatcttatc gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFLAALAA CKPQDNSAAQ AASSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QYRVVSAKI NQKDDSENYL VDHSSGAYLI DNKEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTCCG TACCGCGTTC CTTTGTGCGG GCGGTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CCGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGGTAAGGA AGACATCGGC GCGGATTCA CGCTGACCGA
201 CCGGCAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCAATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTCCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFLAALAA CKPQDNSAAQ VASSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSIDLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QYRVVSAKV NQXDDSENYL VDHSSGAYLI DNKEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFLAALAAACKPQDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFLPGVFLAALAAACKPQDNSAAQAASSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVVV					
g548	GDFTLTDGEGKPFNSDLKGKVVILSFGFTHCPDVCPTGLTYSDTLKQLGGQAKDVVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIVKQYRVVSAKVNQXDDSENYL					
g548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGGQNLPIVKQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180

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	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACTC AAGACAACAG TCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TGCCTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CCGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTACGCA TCGATCCGGA ACGGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAATATTG GTCGACCACT
551 CTTCGGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSEFLP GVFLAALAA CKPQDNSAAQ VASSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSIDLKQL GGQAKDVVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QYRVVSAKV NQKDDSENYL VDHSSGAYLI DNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSEFLPGVFLAALAAACKPQDNSAAQVASSASASAENAAKPQTRGTDMRKEDIG					
a548	MFSVPRSEFLPGVFLAALAAACKPQDNSAAQVASSASASAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVVV					
a548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIVKQYRVVSAKVNQKDDSENYL					
a548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGDQNLPIVKQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

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```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201 cggcagccgt agcgacgca ggcagcaggc gggaaatcgaa cggagtagga
251 atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301 ttcttcggtt acttcttcca tcgccaaatc tgcgcaagca tacacgcagg
351 cgcggttcat ttcttcggtt atggtgggtt cgcgcacatc caacgcgccc
401 cggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451 ggagcgcccg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551 tcgttcatcg tgttcaacat ttcaggcgtc agcaggtttg cgcggagag
601 gccaagaag atgtctttgc cttaaccgc atcgcaagt acgcgcggc
651 cgttgccttc aacggcgtag aatttttttg attcgccat gcggtcttg
701 tcttcgcttc tttggtaaat cagcctttg gagttgcaaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcg
801 cggcacctgc gccggagcac accaaagtcg cttcttcgat tttacggccg
851 gtataacgca gggcggttcaa tacggcgcg gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

g550.pep

```

1 MITDRFHLFH FVSPFIYQSD NKMPPESSD GILTTNGLQL PFAQLGSVSF
51 QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVHLVREV
151 GAAGTDNHVR TGFFRQRRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIIQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

```

1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
51 GTTTGGACTC GTCCATACGG TCTTGTCTT CGCGGGTTTG GTAAATCAGC
101 CCTTTGGAGT CGCAAACGGT CACGTTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGwTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGGCGGCGG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTTGCAG CGTTGCGTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

```

1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows \_\_\_% identity over a \_\_\_ aa overlap with a predicted ORF (ORF 550.ng)

from *N. gonorrhoeae*:

m550/g550

m550.pep				10	20	30
				DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN		
g550				:       : : : : : : : : :		
	190	200	210	220	230	240
m550.pep	40	50	60	70	80	90
	HAFGVANGHVFAFQAQIIQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA					
g550	: : : : : : : : : : : : : : :					
	250	260	270	280	290	300
m550.pep	100					
	VLVVVEYGDFAAFAX					
g550	: : : : : :					
	VLVIMKYGDFAAFAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTGACC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAG ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACGCGCGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
451 CAGCGGCGGC AGGATTTCCG GATTCGGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTTC AGTATTTTTC GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGAGATC GCAAACGGTC
701 ACGTTTTCGC GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTGCTGCTG GAATACGGGG ATTTTGCAGC GTTTCGCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVVFV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGSG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                10      20      30
m550.pep                      DGIGKHALAVVFNGVELFGLVHTVVFVAGL
                                |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVVFVAGL
              170      180      190      200      210      220

              40      50      60      70      80      90
m550.pep    VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG
              |||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG
              230      240      250      260      270      280

              100
m550.pep    RAVLVVVEYGDFAAFAX
              |||
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg catttgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttgcca cggttgctgg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcggtat cgtgagaatg
251 ttttgaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggtea gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```



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451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt  
501 acggcgcatc atctcgcgcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF  
51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT  
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA  
151 LSGKIARHHL PEFTEELRRI ICGGIVD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
151 AATGCCGGAT TTAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA  
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTAT CGTGAGAATG  
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT  
301 TTATTGAAGA ATGCCCGTGA GATATACAG CAAGAAGAAA TTGACGGCAT  
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC  
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGACTGCA  
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCGAGTTTA CGGAAGAGTT  
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG  
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF  
51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT  
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA  
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	:     :     :     :     :     :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	:     :     :     :     :					
g552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	:     :     :     :     :					
g552	YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
151 AATGCCGGAT TTAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA

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```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRIKKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENV	LKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
a552	ALAEMPEAKKDQAAEAFNRYRENV	LKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHL	PEFTEELRRIICGGKNPDAG				
a552	YGSPVGQSVVAKNPRIKKSMSEIAVSWTALSGKIAQHHL	PEFTEELRRIICGGKNPDAG				
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKRHRQKX					
a552	CKQAGQVGKRHRQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51 GTGCACCAAT GCTTTTGCCG CCCGCCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 CCCGGAAGCG AAAAAAGATC AGCGGCAGAG AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCC AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
1 LNIKLTLLLPFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHRQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCCGAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCC AAGTGAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLTLLP PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLKLNAREI YTQEEIDGMI AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLTLLP	PFATLALCTN	AFAAPPSDAS	LARWLDTQNF	DRDIEKNMIE	GFNAGFKPYA
m552-1	LNIKLTLLP	PFATLALCTN	AFAAPPSDAS	LARWLDTQNF	DRDIEKNMIE	GFNAGFKPYA
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEA	KKDQAAEAFN	RYRENVLKDL	ITPEVKQAVR	NTLKLNAREI	YTQEEIDGMI
m552-1	DKALAEMPEA	KKDQAAEAFN	RYRENVLKDL	ITPEVKQAVR	NTLKLNAREI	YTQEEIDGMI
	130	140	150	160	170	180
a552-1.pep	AFYGPSVQGS	VVAKNPRLIK	KSMSEIAVSW	TALSGKIAQH	HLPEFTEELR	RIICGGKNPD
m552-1	AFYGPSVQGS	VVAKNPRLIK	KSMSEIAVSW	TALSGKIAQH	HLPEFTEELR	RIICGGKNPD
	190					
a552-1.pep	AGCKQAGQVG	KRHKQKX				
m552-1	AGCKQAGQVG	KRHKQKX				
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacct gtctttgggc ttgacaaaaa agctgcccgt
51  tatactgcaa acagaagtag cggagtgttg cttggcatgt ctacggctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggttgat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcgggtatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgaaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgttg ccaaacacgc gtttcgaggg aggggaagaa
451 aagcaggaaa tccgcattct acccatgttg cgcgggattt ctgggctggg
501 gcggaatttg tttcagcttt tggttttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctccgaat caggcaaat catgataaat gggcacgaca
701 tttacagctt accgcacct tttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

Computer analysis of this amino acid sequence gave the following results:

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng)

m553/g553

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

1  ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAA AGCTGCCTGT
51  TATCCTGCAG ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
      1  MPHQLNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
      51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRSLSFGFNKKLPVILQTEVAECGLACLT	SILSYYG	FHTDLRTL	RQKYTL	SLKGANL	
	: :   : :     :     : : : : : : :					
a553	MPHQLNLSLGKLPVILQTEISECGLACLA	AVAGFHGFHTNLRALRSKY				
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLTPRALRLEDELSNLQLPCILHWNLNH	FVVLCSISKDSIVIMDP	AVGM			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
      1  atgacagcac ataaaatcct gcccgctcctt cttcccatca tcttaggcgt
     51  ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacg
    101  ccgccccac gctccaaaca cccgaaaccc tcacggcggc acacatcggt
    151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
    201  tgtcgaaccg gcggcactaa cccaactgat gaccgcata tgggttttca
    251  aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaatcccc
    301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccggcga
    351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
    401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
    451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
    501  caccgtattc aaaaacccga caggcttggg tagagaagga caggtttcca
    551  ccgccaagaa cctctccctg ctgtctgaag cattgatgcg cgactttccg
    601  gaatattacc cgctgttttc catcaaatcg ttcaagtttg aaaacataga
    651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
    701  tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
    751  tccggcaacg gcaggcacat ccttgtcatc acactagggt cggaaatcggc
    801  ggaaacccgc gcatcggaca acagcaagct gctgaaccgg gcatgcagg
    851  ccttcgatac gcccacaaata tatccgaaag gcaaaaccgt tgcccaaatc
    901  caaatttccg gaggcagcaa aaaaaccgtc cgcgagggtt tcctcaaaga
    951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
   1001  tggaaaccat acagccgatt cccgccccgg taaaaaagg gcagatttta
   1051  ggaaaaatca aaatcaggca aaacggacat accattgccc aaaaagaat
   1101  cgtcgactg gaaaacgtag aaaaagaag ccggtggcaa aggctttgga
   1151  cgcgtctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
g554.pep..
      1  MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTILQ PETLTAHIV
     51  IDLQSRQTL AKNTNTPVEP AALTQLMTAY LVFKNMKS GN IQSEENLKIP
    101  ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLNGSIE
    151  NFWQOMNKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
    201  EYYPFLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
    251  SGNRHLI VI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
    301  QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
    351  GKIKIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
      1  ATGACAGCAC ATAAATCCT GCCCGTCTG CTTCCATCA TCTTAGCGT
     51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
    101  CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
    151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
    201  TGTGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTCA
    251  AAAACATGAA ATCGGCAAT ATCCAATCTG AAGAAAACCT AAAAATACCC
```

```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTG AAAAACCCTGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAGGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTCATC ACATTGGGTT CGGAATCGGC
801 GGAACACGCG GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AACCGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFQT PETLTAHVIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALTL AGRLGNGSIE
151 NFWQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIIL
351 GKIKIRONGY TIAEKEIVAL ENVKRSRWQ RLWACLQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFQT PETLTAHVIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTLOT PETLTAHVIVIDLQSRQTL					
	10	20	30	40	50	60
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDVS					
	70	80	90	100	110	120
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDVS					
	70	80	90	100	110	120
m554.pep	TDKLLKGMIALSANDAALTLAAGRLGNGSIENFVQMNKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTLADRLGNGSIENFVQMNKEARRLGMKNTVFNPTGLGREG					
	130	140	150	160	170	180
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554.pep	SGGYNLAVSYSGNRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
g554	SGGYNLAVSYSGNRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 . pep  QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIPAVPVKKGQILGKIKIRQNGY
           |||||||||||||||||||||||||||||||||||||||||||||||||||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIPAVPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360

           370      380      390
m554 . pep  TIAEKEIVALENVKKRSRWQRLWACL TGQX
           ||||||||||||:|||||||:|||||
g554      TIAEKEIVALENVKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554 . seq
1  ATGACAGCAC ATAAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCAGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTATCC GCCAAAAACA TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAAACTT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGATC GTCCCGGCGA
351 TCCGGTCAGC ACCGACAAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTGTGTC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCAG CTGTCTGAAG CATTGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTC AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CCTGTCTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554 . pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAHV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMMSGN IRSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALTL AGR LGNGSIE
151 NFVQQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554 . pep  MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQTPETLTAHVIDLQSKQILS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQTPETLTAHVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep  AKNINTPVEPAALTQLMTAYLVFKNMMSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      AKNINTPVEPAALTQLMTAYLVFKNMMSGNIRSEENLKIPESAWASEGSRMFVRPGDTVS

```

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	310	320	330	340	350	360
m554.pep	370	380	390			
a554	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1 atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51 cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatacctgt tgcgcgcgtc atcgtcgccg ccgctgcggg cggctttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1 MDNKTCLRIG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1 ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATTT TACTGACCAC
51 CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1 MDNKTCLRIG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```



101 LSQKCSVDEA HAMFKRPTR QEINQMAAQ SRGQKRPHR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
g556	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
	10	20	30	40	50	60
m556.pep	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
g556	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
	70	80	90	100	110	120
m556.pep	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
g556	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
	70	80	90	100	110	120
m556.pep	QEINQ	MAAQ	SRGQ	KRPH	RX	
g556	QEINQ	MAAQ	SRGQ	KRPH	RX	
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	CGCCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTT	AGCCTCATTA	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG	
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT	
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT	
201	CGACATCGAT	CCCGAAAAAG	GCAGAATCAA	CGAGGCAAAC	CTGCGCCGTA	
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC	
301	CTGTCGCAAA	AATGTTCCGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG	
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC	
401	AGAAACGTCC	GCACCGTTAA				

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT	KLRLG	GLILLT	AVL	SLIIVLIV	DSWPLA	ILLAAV	IVAAAAGGFV
51	WTSRRQ	QRQF	IERLKK	FDID	PEKGRINE	AN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCS	VDEA	HAMFKR	PTR	QEINQMAAQ	SRGQKRPHR	*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
a556	MDNKT	KLRLG	LILLT	AVLSL	IIVLIV	DSWPLA
	10	20	30	40	50	60
m556.pep	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
a556	IERLKK	FDIDPE	KGRINE	ANLRR	MYHSGG	QHOKDA
	70	80	90	100	110	120
m556.pep	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
a556	ATLICS	QKCSV	DEAHAM	FKKR	PTR	
	70	80	90	100	110	120
m556.pep	QEINQ	MAAQ	SRGQ	KRPH	RX	
a556	QEINQ	MAAQ	SRGQ	KRPH	RX	
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pcp..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pcp..

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

a557.seq  
 1 ATGAACAAAC TGTTTCTTAC TGCCGCGATG CTGATGCTGG GCGCGTGC GG  
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA  
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG  
 151 CTGTATCAGG CTTCCGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC  
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC  
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG  
 301 GTATTGAAAC GCGGCGAGCC GGTGCGCAA CCGATGACCG TGTCCTCCG  
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAA CAGGAAGAGG  
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC  
 451 CGCCGCCTGA CCTTTCTGAA GCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep  
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA  
 51 LYQASGRVDD AAGQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ  
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEEALWAE MRQDAAEQIV  
 151 RRLTFLKAE\*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGACGFHL	KGADGISPPL	TYRSWHIEGG	QALRFP	PLETALYQASGRVDD
a557	MNKLFLTA	AVLMLGACGFHL	KGADGISPPL	TYRSWHIEGG	QALQFP	LETALYQASGRVDD
	10	20	30	40	50	60
m557.pep	AAGQMTLRI	DSVSQNKETY	TVTRAAVINE	YLLILTVEAQ	VLKRGE PVGK	PMTVSVRRVL
a557	AAGQMTLRI	DSVSQNKETY	TVTRAAVINE	YLLILTVEAQ	VLKRGE PVGK	PMTVSVRRVL
	70	80	90	100	110	120
m557.pep	AYADNEILGK	QEEEEALWAE	MRQDAAEQIV	RRLTFLKAE	X	
a557	AYADNEILGK	QEEEEALWAE	MRQDAAEQIV	RRLTFLKAE	X	
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq..  
 1 ATGGATGCTT GTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA  
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG  
 201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep..  
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMPLYTFS ELYMLQQGTA  
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP  
 101 LSDGIV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq..  
 1 ATGAATGCTT GTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA  
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG  
 201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

841

m558.pep..  
 1 MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPlyTFS ELYMFQOGTA  
 51 HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP  
 101 LSDGIV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng)  
 from *N. gonorrhoeae*:

m558/g558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPlyTFS	ELYMFQOGTAHQAPHCVLPE				
g558	MDACFFVIPAQAGIRRFIVFKRSGRILAGAGMMPlyTFS	ELYMLQOGTAHQAPHCVLPE				
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSP	LSDGIVX				
g558	RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSP	LSDGIVX				
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

a558.seq  
 1 ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA  
 101 TGCCCTTATA TATAGTGGAT TAAATTTAAA TCAGGACAAG GCGACGAAGC  
 151 CGCAGACAGT ACAAATAGTA CGGCAAGGCG AGGCAACGCC GTACTGGTTT  
 201 AAATTTAATC CACTATACTT TCTCCGAGCT TTATATGTTT CAACAGAGGA  
 251 CGGCACATCA AGCACCGCAC TCGTGTTGTC CCGAACGAGA CTGCCCTCCG  
 301 ATTAGATTCT ATCGCTATAA ACAGACGGGT TTCAACCGAA AAGGAATGGG  
 351 AATGAAGTCC GTTCCGACA CCTCTCGGGC GATGCCGTCT GAAAACCAAT  
 401 CTCCACTTTC AGACGGCATT GTTTAG

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pep  
 1 MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPlyIVD \*I\*IRTRRRS  
 51 RRQYK\*YGKA RQRTGLNLI HYTFSELYMF QQRTAHQAPH CVLPERDCPP  
 101 IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPLSDGI V\*

m558/a558 70.2% identity in 141 aa overlap

	10	20	30			
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPly	-----				
a558	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPly	IVDXIXIRTRRRSRRQYKXYGKA				
	10	20	30	40	50	60
	40	50	60	70	80	
m558.pep	-----TFSELYMFQOGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS					
a558	RQRTGLNLIHYTFSELYMFQOGTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS					
	70	80	90	100	110	120
	90	100				
m558.pep	ISDIXRAMPSENQSP	LSDGIVX				
a558	VSDTSRAMPSENQSP	LSDGIVX				
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

g560.seq  
 1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAKHQSGW ETALQEIFP PQVYVAKREL
101 FKIPFGWGWL KLVKTIIDIR NMRREANEQL IKQGLARKNE GXYWITFPEG
151 TRLAPGKRGK YKLGGARMAC MFREMDIVPA LNSGGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAEIMEK CEHLIETOOP LISGAGPFPA EMPSET*

```

m560.seq

1	ATGCTCATCA	TCCGCAACCT	GATTTACTGG	CTGATACTCT	GTTCCACCCT
51	GATTTTCCTC	TTTCCCTTTA	TGCTGCTCGC	CTGCCTTTC	CGGGACGGGG
101	CGCACAAAGAT	GGCGCGGGTC	TGGGTCCGGA	TTCTCAACTG	GTCGCTCAAA
151	CACATCGTCG	GGCTCAAATA	CGGCATCATC	GGCGCGGAA	ACATCCCCGA
201	CGCCGCCGCC	GTCATCTGCG	CCAAACACCA	AAGCGCTTGG	GAACAGCTCG
251	CCCTTCAGGA	GATTTTTCGG	CCGCAGGTTT	ACGTTGCCAA	ACGCGAGTTG
301	TTCAAATCC	CCTTTTTCGG	CTGGGGCTTG	AAACTGGTCA	AAACCATAGG
351	CATAGACCGC	AACAACCCGC	GCGAAGCCAA	CGAGCAGTCT	ATAAAACAGG
401	GGTTGGTGCG	CAAAAACGAA	GGCATTTGGA	TTACCAATTT	CCCCGAAGGC
451	ACGCGCCTTG	CGCCCGGAAA	ACGCGGCAAA	TACAAACTCG	CGCGCGCGCG
501	CATGGCGAAA	ATGTTTGAGA	TGGACATCGT	CCCCGTCGCC	CTCAACACGG
551	GCGAATTTTG	GCCGAAAAAC	TCCTTTCTGA	AATATCCGGG	GGAATCACC
601	GTCGTCATCT	GTCGACCATC	CCGACACGCA	AGCGGCAGCG	AAGCCGAATT
651	GATGGAAAAA	TGCGAACATC	CTCATAGAAA	GCAACAACCG	CTTATTTCCG
701	GCGCAGGCCC	GTTTGGCGCC	AAAATGCCGT	GTGAAACCGC	ATGA

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV VVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWTITFPEG
151 TRLAPGKGRK YKLGGARMAC MFEMDIVPVA LNSGEFWPKN SFLTKYPEGIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETOPA LNSGAGPFPA KMPSETA*

```

Homology with a predicted ORF from *N.gonorrhoeae*

from *N. gonorrhoeae*:

m560/g560

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFFPMLLASPFDRGAHKMARVWVGILNWSLKHIVGLKYRII					
	:					
g560	MLIIRNLIYWLILCSSLIFLFFPMLLASPFDRGAHKMARVWVGILNWSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	:					
g560	GAEHIPDRPSVICAKHQSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```
a560.seq
1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTGCGCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AACTGGTCA AAACCATAGG
351 CATAGCCGC AACAAACGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGCGCG CAAAACGAA GGCTATTGGA TTACCATTTC CCCCAGGCG
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TCGGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCGG
701 GCGCAGGCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```
a560.pep
1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHSGW ETALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*
```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
a560	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPA VICAKHSGW ETALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR					
a560	GAENIPDRPA VICAKHSGW ETALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

844

	130	140	150	160	170	180
m560.pep	190	200	210	220	230	240
	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPF	FAA				
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMGKCEHLIETQQPLISGAGPF	FAA				
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

m561.seq.

```

1   ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTCGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACAA TCGAACTGTT TTTGCAGGCA
451 TTGGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTGCTC TGTACTGATG CTGTTTGGC
551 ACCAGATTTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTCCTA TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCGG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTTG GGAAGTACC ATGAGGAAAT CTTCCCATG GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAACCG CATTTCCTTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGCACAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
1251 CGAAAACAAA CGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTCCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTTCT GCCGCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGCCAACAT CCGCAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCCAC GGGCAGCCAT
1651 GTCGGAATGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCAAGCTC AACAGGAAC CACCGTCTCA TTGACGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m561.pep

```

1   MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEQNQNLTLY LYOTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFAENK REEAAENISF IKTGVQECYE DVRELLLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMIFIL

```

845

501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFD T EKIGEPTGSH  
 551 VGLHIMQERA KRIHAVLEIR SQAQQGTTVS LTVASEESLK \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLVWGLAALS	VVLTLLLSRL	LENAASVIEEAGNL	RMQAY		
g561	MILPTRFSDGIPLSRLKLLTGLVWGLAALS	VVLTLLLSFRL	LENAASVIEEAGNL	KMQAY		
	10	20	30	40	50	60
m561.pep	RLAYMAGEGSPRAQIDNQVAEF	EKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAEF	EKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEF	EKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAEF	EKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
m561.pep	HILPPLQSYRRPTQVDLYRFAGN	IELFLOALENANEKNTWWLRR	FQWAIMLMTLVSSVLM			
g561	NILPPLQAYRRPTQIELYRFAGN	IELFLOALENAGEKNTWWLRR	FQWVIMLMTLVSSVLM			
	130	140	150	160	170	180
m561.pep	LFWHQIWVIRPLQALREGAERIG	RRCFDIPVPEGGTPEFKQVGR	CFNQMGGR	LKILYDDL		
g561	LFWHQIWVIRPLQALREGAERIG	RHRFDIPVPEDVRPNSNRSG	GVSTKWRSGX			
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIG	RRCFDIPVPEGGTPEFKQVGR	CFNQMGGR	LKILYDDL		
g561	LFWHQIWVIRPLQALREGAERIG	RHRFDIPVPEDVRPNSNRSG	GVSTKWRSGX			
	190	200	210	220	230	
m561.pep	EGQVAEQTRSLEKQONLTLTYQT	TRDLHQSYIPQQA	AHFLNRILPAVGADSGR	VCCLDG		
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCTT
301	TCGGACACCC	CTCTTGCTTA	TGATTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAACTGTT	TTTGCAGGCA
451	TTGGAATATG	CCAACGAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCGTC	TGTACTGATG	CTGTTTGGC
551	ACCAGATTGG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTGG	GAAGGACAAG	TCGCGGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAATCAAAA	CCTGACCCCTG	CTGTACCAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCCGATTGG	GGGAAGTACC	ATGAGGAAAT	CTTCCCAT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCTG	CTTGACAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCTTTGCG
1251	CGAAACAAA	CGGAGGAAG	CCGCAGAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCTGAA	GCCGTTGCCG	ACCTATTCTC



```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

a561.pep

```

1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51 EAGNLRMQAY RLAYMAGEGS PRAQIDNOVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIHWIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLTLYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDT ENIGEPSGSH
551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

```

m561/a561 96.9% identity in 590 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	SVVLTLLLSLRL	LENAASVIEE	EAGNLRMQAY		
a561	MILPARFSDGISLSRLKLLTGLWVGLAALS	SVVLTLLLSLRL	LENAASVIEE	EAGNLRMQAY		
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNOVAEFEKSLKRIA	QSDAIHPLIP	SDTPLAYDLI	QSMLIIDWQA		
a561	RLAYMAGEGSPRAQIDNOVAEFEKSLKRIA	QSDAIHPLIP	SDTPLAYDLI	QSMLIIDWQA		
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQA	LENANEKNTW	WLRRFQWAIM	LMTLVSSVLM		
a561	HILPPLQSYRRPTQVDLYRFAGNIELFLQA	LENANEKNTW	WLRRFQWAIM	LMTLVSSVLM		
	190	200	210	220	230	240
m561.pep	LFHWQIHWIRPLQALREGAERIGRRCFDIP	VPEGGTPEFK	QVGRCFNQM	GGRLLKILYDDL		
a561	LFHWQIHWIRPLQALREGAERIGRRCFDIP	VPEGGTPEFK	QVGRCFNQM	GGRLLKILYDDL		
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQ	SYIPQAAEH	FLNRILPAVG	ADSGRVCLDG		
a561	EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQ	SYIPQAAEH	FLNRILPAVG	ADSGRVCLDG		
	310	320	330	340	350	360
m561.pep	GSDVYVSIHHADCGTAASDLGKYHEEIFPI	EYQNETLGRLLS	FNGISL	DEDDRILLQT		
a561	GSDVYVSIHHADCGTAASDLGKYHEEIFPI	EYQNETLGRLLS	FNGISL	DEDDRILLQT		
	370	380	390	400	410	420
m561.pep	LGRQLGVSLAGAKQEEKRL	LAVLQERNLIA	QGLHDSIAQ	ALTFLNLQVQ	MLETAFENK	
a561	LGRQLGVSLAGAKQEEKRL	LAVLQERNLIA	QGLHDSIAQ	ALTFLNLQVQ	MLETAFENK	

847

	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
m561.pep	490	500	510	520	530	540
	WENGSLPFPQEAQLQMIFILQESLSNIRK HARATHVKFTLSEHGGRFTMTIQDNGQGFD					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRK HAATHIKFRLKQDGSFTMTIQDNGQGFD					
	490	500	510	520	530	540
m561.pep	550	560	570	580	590	
	EKIGEP TGS HVGLHIMQERAKRIH AVLEIRSQAQQGTTVSLTVASEESL KX					
a561	ENIGEP SGSHVGLHIMQERAKRIH AVLEIRSQAQQGTTVSLTVASEESL KX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1  atggcaagcc cgctcagtcct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc ggcgcggttt tggtcggaat catgttttcc acgcgcgtgc
101 gggcgcgccg caggtcctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggatcatgtcg gcggtcagga cgctgtcggt caccgcgtac
301 acgacggttg catcgacatc gtcgccgccc ggtgcggaat tgaggacttt
351 tttcgcgcgg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tcggggtcga gaagaagggg attttgcgcg cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcgttg
601 acggcgacga tttgagattg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSTFPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMR LPSWDTSASKR PCTVSNLVRW ALVSRPLPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCCGCGCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TGCGGGTCGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGTGAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNT LATGERQLVV QEALTTVMS AVRTLSTFPY

```

848

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS  
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL  
 201 TATSWSWS\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSG	STKPTAFAAPVL	VGIMFSTPLRARRR	SLWRTSVTVWSL	VS	SAWMVVIAP
g562	MASPSSLPFNSG	STKPTAFAAPVL	VGIMFSTPLRARRR	SLWRTSVTVWSL	VS	SAWMVVIAP
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMP	TL	SLNTLATGERQL	VVQEALETTVMS	AVRTLSFTPYTT	VASTSSPPGAEMRTFFAP
g562	LTMP	TL	SLNTLATGERQL	VVQEALETTVMS	AVRTLSFTPYTT	VASTSSPPGAEMRTFFAP
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLL	VNAPVHSMTKSTP	SSFHGS	SAGLRVEKKGIL	SPLTMLRPP	SWDTASAKR
g562	LSRWILAFSLL	VNAPVHSMTKSTP	SSFHGS	SAGLRVEKKGIL	SPLTMLRPP	SWDTASAKR
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRW	ALVSRLPLALT	TATSWSWSX			
g562	PCTVSNLVRW	ALVSRLPLALT	TATWSWSX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq  
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC  
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC  
 101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG  
 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTC  
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT  
 251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC  
 301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT  
 351 TTTCGCGCCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG  
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT  
 451 TCGGCAGGGT TCGGGTCNA GAAGAANGG ATTTTGTGCG CGTTGACGAT  
 501 GAGGTGCGCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACGCG  
 551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG  
 601 ACGGCGACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep  
 1 MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL  
 51 VSAWMVVIAP LTMP

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSG	STKPTAFAAPVL	VGIMFSTPLRARRR	SLWRTSVTVWSL	VS	SAWMVVIAP
a562	MASPSSLSFN	SGSTKPTAFAAP	VLVGIMFSTPLRARRR	SLWRTSVTVWSL	VS	SAWMVVIAP
	10	20	30	40	50	60

	70	80	90	100	110	120
m562.pep	LTMP	TL	SL	N	L	A
	T	G	E	R	Q	L
	V	V	Q	E	A	L
	E	T	T	V	M	S
	A	V	R	T	L	S
	F	T	P	Y	T	T
	V	A	S	T	S	S
	P	P	G	A	E	M
	R	T	F	F	A	P
a562	LTMP	TL	SL	N	L	A
	T	G	E	R	Q	L
	V	V	Q	E	A	L
	E	T	T	V	M	S
	A	V	R	M	L	S
	F	T	P	Y	T	T
	V	A	S	T	S	S
	P	P	G	A	E	M
	R	T	F	F	A	P
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSR	W	I	A	F	S
	L	V	N	A	P	V
	H	S	M	T	K	S
	T	P	S	S	F	H
	G	S	S	A	G	L
	R	V	E	K	K	G
	I	L	S	P	L	T
	M	R	L	P	P	S
	W	D	T	S	A	S
	K	R				
a562	LSR	X	T	L	A	F
	S	L	V	N	A	P
	V	H	S	M	T	K
	S	T	P	S	S	F
	H	G	S	S	A	G
	L	R	V	X	X	G
	I	L	S	P	L	T
	M	R	L	P	P	S
	W	D	T	S	A	S
	K	R				
	130	140	150	160	170	180
	190	200	209			
m562.pep	P	C	T	V	S	N
	L	V	R	W	A	L
	V	S	R	L	P	L
	A	L	T	A	T	S
	W	S	W	S	X	
a562	P	C	T	V	S	N
	L	V	R	W	A	L
	V	S	R	L	P	L
	A	L	T	A	T	I
	W	S	W	S	X	
	190	200				

g563.req

1	ATGAACAAAA	CCCTCTATCG	TGTGATTTC	AACCGCAAA	CGGGTGC
51	GGTAGCTGTT	GCCGAAATCA	CCAAGCGCGA	AGGTAAAAGC	TGTGCCGATA
101	GTGGTTTCGG	CAGCGTTTAT	GTGAAATCCG	TTTCTTTTCA	TCCTATCTCA
151	TCCAAGGCCT	TTTGTTTTTT	TGCATTATGG	TTTTCTTTAT	TTGTGGCTTT
201	GGGTACGGTC	AATATTGCTT	TTGCTGACGG	CATTATTACT	GATAAAGCTG
251	CTCCTAAAAC	CCAACAAGCC	ACGATTCTGC	AAACAGGTAA	CGGCATACCG
301	CAAGTCAATA	TTCAAACCCc	tACTTCGGCa	ggGGTTTCTG	TTAATCAATA
351	TGCCCAGATT	GATGTGGGTA	ATgcGGGGC	GATTTTAAAC	AACAGTCGCA
401	GCAACACCCA	AACACAGCTA	GGCGGTTGGA	TTCAAGGCCA	TCCTTGGTTG
451	ACAAGGGGCG	AAGCACGTGT	GGTGTGTAAC	CAAAACAACA	GCAGCCATCC
501	TTCACAACCT	AATGGCTATA	TTGAAGTGGG	TGGACGACGT	GCAGAAGTCG
551	TTATTGCCAA	TCCGGCAGGG	ATTGCAGTCA	ATGGTGGTGG	TTTTATCAAT
601	GCTTCCCCTG	CCACTTTGAC	GACAGGCCAA	CCGCAATATC	AAGCAGGAGA
651	CTTTAGCGCG	TTTAAGATAA	GGCAAGGCCA	TGCTGTAATC	CGCGGACACG
701	TTTTGGATGC	CCGTGATACC	GATTTACAC	GTAATCTTTT	GATTGCCAAC
751	AAAATCACCT	TGATCAGTAC	GGCCGAACAA	GCAGGCATTG	GTAATCAAGG
801	GCAGTTGTTT	GCTTCTTCCG	GTAATGTGGC	GATTGATGCA	AATGGCCGTT
851	TGGTCAATAG	TGGCACGATG	GCTGCCGCCA	ATGTGCAAGA	TATGAATTAAT
901	ACAGCGGAAC	ACAAAGTCAA	TATCCGCAAT	CAAGCCTTTG	AAAACAGCGG
951	TACGCGGGTA	TCCGAACAAG	GCACTCAAA	TCACAGTCAA	TCGATTCAAA
1001	ACACTGGCAA	ATTATTGTCG	GCAGGAACAG	AGGATTTAGC	CGTTTCAGGC
1051	AGCCTGAACA	ATCAAAATGG	CGAAATAGCG	ACCAATCAAC	AACTGATTAT
1101	TCACGATGGT	CAGCAATCTA	CCGTTGTTCAT	TGATAATACG	AATGGCACGA
1151	TACAATCAGG	CCGTGATGTT	GCCATTTCAG	CAAAATCGTT	ATCCAACAAC
1201	GGCACAACCT	CGCGTGATAA	TAAACTGGAT	ATTGCGTTAC	AAGATGATTT
1251	TTATGTAGAA	CGCAAGATCG	TGGCGGGCAA	TGAATTGTCT	CTCAGTACAC
1301	GAGGCAGCCT	GAAAAATTCA	CATACCTTGC	AAGCAGGAAA	ACGCATTCCG
1351	ATTAAGGCAA	ATAACCTTGA	TAATGCAGTA	CAAGGCAACA	TTCAATCCGG
1401	CGGTACGACA	GACATTGGCA	CGCAGCACAA	TTTAACCAAT	AGAGGCTTGA
1451	TTGACGGACA	ACAAACGAAA	ATCCAAGCCG	GGCAAAATGAA	TAATATTCCGT
1501	ACAGGTCGGA	TTTATGGCGA	CAATATTCGT	ATTGCGGGTA	CCCGCTTAGA
1551	CAATCAAGAT	GAAAACGGTA	CAGGTGCCGC	CATTGCGGCA	CGCGAAAACC
1601	TGAATTTAGG	CATTGAACAA	TTAAATTAACC	GTGAAAACAG	TCTGATTTAC
1651	AGCGGTAACG	ATATGGCGGT	TGGCGGCGCA	TTGATACCA	ATGACCAGAC
1701	CACAGGCAAA	GCCCAATAGG	TACACAAATG	CGCGCAATC	ATTGAAGCTG
1751	CAGGCAAAAT	CGGTTTAGGT	TAGAAAAGC	TGCACAATAC	CAATGAGCAT
1801	TTGAAAACGC	AGTTGGTAGA	AACAGGGCGC	GAGCGTATTG	TTGATTACGA
1851	AGCATTTGGA	CGACACGAAT	TATTGCGAGA	AGGCACGCAA	CATGAATTAG
1901	GCTGGTTTGT	CTACAACAAT	GAATCAGACC	ACTTACGCAC	CCCTGATGGA
1951	GTGGCGCATG	AAAATTGGCA	TAAATACGAT	TATGAAAAAG	TAACGCAAGA
2001	AACTCAAGTA	ACCGGAACCT	CGCGTGCTAA	AATCATTGCA	GGTAGCGGAT
2051	TGATTATTGA	TAGCAAAGCA	GTCTTCAACA	GCGACAGCCG	AATCATTGCC

2101 GGCGGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA  
2151 AACCTTTGGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAAC  
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA  
2251 AATTATACTT TGCCGGAGGA AATCACACGC GACATTTCAC TGGGTTTCATT  
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG  
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TCGGAAAAGC  
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG  
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA  
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGTAG TGAATATATG  
2551 CTGGGCAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA  
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG  
2651 GGATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC  
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG  
2751 CATTGCAATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT  
2801 GGTGGGTACA AAAAGAAGTT AAACCTCCTG ATGGCGGCAC ACAAACCGTA  
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA  
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC  
2951 TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC  
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT  
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC  
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC  
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC  
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG  
3251 GCAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA  
3301 GGGCAAAACC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA  
3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC  
3401 GAGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT  
3451 ACCCTatTGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG  
3501 CGCAAAAGGC ACACCTGCCG TGTATGCTAA AAATGACATT ACTATCAGCT  
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAACA TACAGGCAGA  
3601 AGCGGCGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA  
3651 CGAAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG  
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTC CGATAATGGC  
3751 ACCCGGATTC AAGCAGGCAA TCATGTTGCG ATTGGTACAA CCCAAACTCA  
3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG  
3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAAACCA  
3901 TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCC TGAAAGGCGA  
3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAACCGGC AGCAACGTTT  
4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAGTAT GGATATTGGC  
4051 GCAGCACAAA ACCAATTAAA CAGCAAAACC ACCCAAACCT ACGAACAAAA  
4101 AGGCTTAACG GTGGGCATTG AGTTCGCCG TTACCGATTG GGCACAACAA  
4151 GCGATTGCCG TAGCACACAA AGCAGCAAAAC AAGTCGGACA AAGCAAAAAC  
4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTTGGC AGGCCTATCA  
4251 AACAGGCAAA GGCGCACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAC  
4301 AAGTCAGCAT CTCCATAACC TACGGCGAAC AGCAAAACCG ACAAAACACC  
4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAG CAGGCGGCAA  
4401 AACTACCTT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA  
4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG  
4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA  
4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTG GGACAAGGAG  
4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTGCGCAA AGGCTACGGC  
4651 TATGGCGATA GCGTAAACCCA CCGCCATAGC CATATTGGCG ACAAAGGCAG  
4701 CCAAACCTT ATCCAAAGTG GTGGCGATAC CATCATCAA GGCAGCAAG  
4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT  
4801 GTACAAGATA GAGAACTTA TCAAAGCAAA CAACAAAACG CCGGTGCACA  
4851 AGTTACCGTA GGTATGGCT TCAGTGCCAG TGGCGATTAC AGCCAAAGCA  
4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC  
4951 GGAGAAAGAC GCTATCAAAT CAAGTCCGA AACCATACAG GCCTCAAAGG  
5001 CGGCATCATC ACCAGCAGCC AAAGCGCAA AGACAAGGGT AAAAACCGAT  
5051 TCAGCACAGG CACACTCGCC GGCAGTGATA TTCAAATTA CAGCCAATAC  
5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC  
5151 ACTGGGACAG GGCGCAAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA

5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC  
 5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT  
 5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCCG  
 5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA  
 5401 CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG  
 5451 TGAACCTGGAT TTACAAAgaa CCGTCAGCCA AGATTTTAGT AAAAATGTTC  
 5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC  
 5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT  
 5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG  
 5651 CAGATAATTG GCAACAAGGC AAAGTCATT CCAACATGTT AGCCTCAGGT  
 5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC  
 5751 GCCagaCGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC  
 5801 AAAACGCGAA TGGCAAACCT ACCGCCAGTC AagaAACCCG TCACGTTCTT  
 5851 GCCCACGCGG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC  
 5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggc CCCCCAATCA  
 5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcggag  
 6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggt a cGgctGCCGG  
 6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa  
 6101 cggctTCaga TTTGCTTCC TCTTTTTCAT ATCTATAAA CATGTGA

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pcp..

1 MNKTLRVIF NRKRGAVVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH  
 51 SKAFCSFALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNGIP  
 101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL  
 151 TRGEARVVVN QINSSHPSQL NGYIEVGRRR AEVVIANPAG IAVNGGGFIN  
 201 ASRATLTGQ PQYQAGDFSG FKIRQNAVI AGHGLDARDT DFTRILLYAN  
 251 KITLISTAEQ AGIRNQQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN  
 301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG  
 351 SLNNQNGEIA TNQQLIIHDG QOSTVVIDNT NGTIQSGRDV AIQAKSLSNN  
 401 GTLAADNKL DIALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR  
 451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQQTQ IQAGQMNIG  
 501 TGRIYGDNIA IAATRLDNQD ENGTGAIAIA RENLNLGIEQ LNNRENSLIY  
 551 SGNDMAVGG A LDTNDQATGK AQRIHNAGAI IEAAGKMRLG VEKLHNTNEH  
 601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWVFNYN ESDHLRTPDG  
 651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA  
 701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNWYRARRK GHDETGHREQ  
 751 NYTLPEBITR DISLGSFAYE SHSKALSRHA PSQGTLPQS NRDNIRTAKS  
 801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGS DYM  
 851 LGSCLKDPNN LHKRLGDGYY EORLINEQIA ELTGHRRLDG YONDEEQFKA  
 901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV  
 951 LMPQVYVRVK NGGIDGK GAL LSGSNTQINV SGSLKNSGTI AGRNALIINT  
 1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTLNNA GNNINNQSTA  
 1051 KSSQNAQSS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ  
 1101 GQTRLQAGRD INLDTVQTGK YQEIHFADN HTIRGSTNEV GSSIQTGKDV  
 1151 TLLSGNNLNA KAAEVGSAKG TLAVYAKNDI TISSGIHAGQ VDDASKHTGR  
 1201 SGGGNKLVI DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG  
 1251 TRIQAGNHVR IGTQTQSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ  
 1301 SQSNEHTGST VGSCLKGDTTI VASKHYEQTG SNVSSPEGNN LISTQSMIDG  
 1351 AAQNQLNSKT QTQYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVQSKN  
 1401 DRVNAMAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQRQT  
 1451 QVQANQAAQS QIQAGGKTTL YCRRCEQSN INITGSGVSG RAGTGLIADK  
 1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGGWSLGVA AGGNVKGKYG  
 1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTI IK GAQVRGKGVQ VNAKNLSIQS  
 1601 VQDRETYQSK QQNAGAQT V GYGFSASGDY SQSKIRADHA SVTEQSGIYA  
 1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFTGT LA GSDIQNYSQY  
 1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LTIADKNGA SSSVGYGSDS  
 1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTDTAE  
 1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNT EI NQHLDKLKAD  
 1851 KEAAETA AAE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG  
 1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQNANGKL TASQETAHVL  
 1951 AHAVLGAAVA AAXGNNAPAG ALGAGGSEAA APIIGKWLYG KGDGGS LNAE  
 2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

```

1  ATGAATAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATTG
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAACGGCA TACCGCAAGT CAATATTCAA ACCCTTACTT CGGCAGGGGT
351 TTCTGTTAAT CAATACGCCC AGTTTGTATG GGGTAATCGC GGGGCGATTG
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAATCCTT GGTTCGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTAA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA CGGCGTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCGTG ATACCGATTG CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTCG
801 TGTGCTCGCG GGACAAAACG ATGTGGTCGC AACAGGTAAT GCACATTTCG
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TGCGATTGAT ACAGGCAAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATTC
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCGAAAGA
1101 TACGGATAAT ACAGCGGAAC ACAAGTCAA TATCCGAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA AACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTGCGGC AGCCTGAAAA ATGAAACATC AGGCACCATT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC AACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAATCTCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACC CGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATTC ATCCACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAACTGCG CCTACCTTTG CTGATGGGAC AATTCGCACT CATGGTGAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTCATC AGTTAAATGC
1701 AAAAGGTTTG CGGTTTGACA ATCACAATGG AACAATTATC AGTGATGCGG
1751 TCCACATTCA AGCCGGCAGC CTGAATAATC AAAATGGCAA CATCACAACA
1801 CGCCAACAGT TAGAGATTGA AACCGATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTG TTATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCT CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTCCG ATTAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACCAAA ATCCAAGCCG GGCAAAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
2451 CATCGGACAA TTAAACAACC GTGAAAACAG TCTGATTTAC AGCGGTAACG
2501 ATATGGCCGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAAGGA TACACAATGC CGGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTTGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
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2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAAA AACCCAAAGT
2851 ACCCAAACCTG CGCCAGCCAA AATCATTTCA GGTAATGATT TAACCATTGA
2901 TTGTTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
2951 TCATTGTACA AACAGAAAAA GACGGTTTGC ATAACGAGCA AACCTTTGGC

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3001 GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA  
3051 GAAACATAAA GGACGAGACT CAACGGGACA TAGCGAACAA AATTACACTT  
3101 TGCCGGAGGA AATCACACGC AACATTTCAC TGGGTTCAAT TGCCTATGAA  
3151 TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT  
3201 GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC  
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT  
3301 CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG  
3351 TGAATATATG CTGGACAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC  
3401 GTTTGGGTGA TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA  
3451 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA  
3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC  
3551 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC  
3601 GATATGTTT GGTGTTGACA AAAAGAAGTT AAGCTTCTCG ATGGCGGCAC  
3651 ACAAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA  
3701 TAGACGGTAA AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT  
3751 TCAGGCGACC TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT  
3801 TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA  
3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT  
3901 TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA  
3951 AAGCACCAACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG  
4001 ACCGAATGGC AGGTATTTAT ATCAGAGGCA AAGAAAAAGG TGTTTTAGCA  
4051 GCGCAGGCAG GAAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA  
4101 ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG  
4151 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC  
4201 CATGTTATTC GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA  
4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG  
4301 AAGTCAGCAG CGCAAACGGT ACACTCGCTG TGTCTGCCAA AAATGACATC  
4351 AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA  
4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC  
4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT  
4501 GTATTGCAAG CAGGAAACGA TGCCAACATC CTGGCAGCA ATGTTATTTT  
4551 CGATAATGGC ACCCAGATTC AAGCAGGCAA TCATGTTCCG ATTGGTACAA  
4601 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA  
4651 TTGATGAGTG CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA  
4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT  
4751 TGAAAGCGCA TACCACCAT GTTGCAAGCA AACACTACGA ACAAATCGGC  
4801 AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT  
4851 AGACATTCAA GCGGCACACA ACAAATTAAA CAGTAATACC ACCCAAACCT  
4901 ATGAACAAA AGGCCTAAG GTGGCATTCA GTTCGCCGT TACCGATTG  
4951 GCACAACAAG CGATTGCCGT AGCACAAGC AGCAAACAAG TCGGACAAAG  
5001 CAAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG  
5051 CCTATCAAAC AGGTAAGAGT GCACAAACT TAGCCAATGG TACAACCAAT  
5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GCGGAACAGC AAAACCGACA  
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAGCAG  
5201 GTGGTAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC  
5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC  
5301 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG  
5351 GCCAAACAAT ATCGGCAGGC TGGAACGCAG GTGCTGCCGT ATCATTGCGA  
5401 CAAGGAGGCT GGTCAATTAG CGTTACCGCA GCGGCAATG TCGGCAAAGG  
5451 CTACGGCAAT GCGACAGCA TCACCCACCG CCATAGCCAT ATCGGCAGCA  
5501 AAGGCAGCCA AACCCCTTAT CAAAGCGGTG GCGACACTAC CATCAAAGGC  
5551 GCGCAAGTAC GCGGCAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT  
5601 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACA CAAAACGCCA  
5651 GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGTTGG CGATTACAGC  
5701 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT  
5751 TTATGCCCGA GAAGACGGCT ATCAAATCAA GGTGCGAAAC CATAAGACC  
5801 TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA  
5851 AACCGCTTTC AGACGGCCAC CCTCACCCTAT AGCGACATCA AAAACACAG  
5901 CCAATACAAA GCGGAAAGTT TTGGATTGGG CGCAAGTGCG TCCTAAGCG  
5951 GCAAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG  
6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG  
6051 CGACAGCGAC AGTCAAAGCA GCATCAGAAA AAGCGGCATC AACACCCGCA



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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGCAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAAGT GGATTTACAA AGAACCCTCA GCCAAGATTT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
6601 GGTCAAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGGCG GGTCCGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CGGCAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGCGGC AGTCGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAAATT TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTG
7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAATAACCA
7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAGAAAA AGATTATCTG AAAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACTT AGATAATACT GGTGCCGGAT TTAAAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

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1 MNKTLRYVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVFPGTTH
51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTQQATILQT
101 GNGIIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRNN TQTQLGGWIQ
151 GNPWLARGEA RVVVNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHSKIADP VWGQDVRVVA QONDVVATGN AHSPILNNA ANTNNNTANN
301 GTHIPLFAID TGKLGGMVAN KITLISTAEQ AGIRNQGLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVNSGTAV SQQTQIHSQ
401 SIQNTGTLIS SGEILIHNSG SLKNETSGETI EAARLAIDTD TLNNQGLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSST
501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQGLEIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNOQLIHDG
651 QNGTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTGAIAIA RENLNLGIGQ LNNRENSLIY SGNDMAVGA LDITNGQATGK
851 AQRIHNAGAT IEAAGKMLRG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWRKHKH GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGSDDY LDSLKLDPNN LHKRLGDGYY EQRLINEQIA
1151 ELTGHRRLDG YQNDDEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQSAVTAT QDINNIGGML
1301 SAEQTLILLNA GNNINSQSTT ASSQNTQSS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AGQISNQSEQ QOTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGDV TLLSGNNLNA KAAEVSSANG TLAWSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TOIQAGNHVR IGTQTQTSQS ETYHQTKQSG

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### Homology with a predicted ORF from *N.gonorrhoeae*

m563/g563

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10      20      30      40      50
g563.pep MNKTLRVVIFNRKRGAVVAVAETTKREGKSCADSGSGSVVYKSVSFIPTH-----SKAFC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep MNKTLRVVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
10      20      30      40      50      60

60      70      80      90      100     110
g563.pep FSALGFSLCLALGTVNIAFADGIITDKAAPKTQQATILQTNGNIPQVNIQTPTPSAGVSVN
|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep FSLLGFSLCLAVGTANIAFADGIADKAAPKTQQATILQTNGNIPQVNIQTPTPSAGVSVN
70      80      90      100     110     120

120     130     140     150     160     170
g563.pep QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
130     140     150     160     170     180

180     190     200     210     220     230
g563.pep VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVIAAGHGL
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVIAAGHGL
190     200     210     220     230     240

240
g563.pep DARDTDFTRIL-----
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAANTSNNNTANN
250     260     270     280     290     300

250     260     270     280     290
g563.pep -----LYANKITLISTAEQAGIRNQGLFASSGNVAIDANGRLVNSGTM
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
m563.pep GTHIPLFAIDTGLKGGMYANKITLISTAEQAGIRNQGLFASSGNVAIDANGRLVNSGTM
310     320     330     340     350     360

```

	300	310	320	330	340	
g563 . pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----					
	::: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m563 . pep	AAANAKDNTNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTTLLSSGEILIHNSG					
	370	380	390	400	410	420
-----						
g563 . pep						
m563 . pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTGSQKLHIDAQGMKNRGRMGLQDTAPTAS					
	430	440	450	460	470	480
-----						
g563 . pep						
m563 . pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSI SNITAPT FADGTIRTHGALDNSGSI					
	490	500	510	520	530	540
-----						
g563 . pep						
m563 . pep	IANGQTDVSAQQGLNNAGQIDIHQ LNAKGSAFDNHN GTI ISDAVHIQAGSLNNQNGNITT					
	550	560	570	580	590	600
-----						
			350	360	370	380
g563 . pep	-----EDLAVSGSLNNQNGE IATNQQLI IHDGQQSTVVIDNT					
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m563 . pep	RQQLEIETDQLDNAHGKLLSAE IADLAVSGSLNNQNGE IATNQQLI IHDGQQSTAVIDNT					
	610	620	630	640	650	660
-----						
	390	400	410	420	430	440
g563 . pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS					
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m563 . pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS					
	670	680	690	700	710	720
-----						
	450	460	470	480	490	500
g563 . pep	HTLQAGKRIRIKANNL DNAVQGNIQSGGTTDIGTQHNL TNRGLIDGQQT KIQAGQMNNIG					
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m563 . pep	HTLQAGKRIRIKANNL DNAAQGNIQSGGTTDIGTQHNL TNRGLIDGQQT KIQAGQMNNIG					
	730	740	750	760	770	780
-----						
	510	520	530	540	550	560
g563 . pep	TGRIYGDNIAIAATRLDNQDENG TGA AIAAREN LNLGIEQLNNRENSLIYSGNDMAVGGA					
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m563 . pep	TGRIYGDNIAIAATRLDNQDENG TGA AIAAREN LNLGIGQLNNRENSLIYSGNDMAVGGA					
	790	800	810	820	830	840
-----						
	570	580	590	600	610	620
g563 . pep	LDTNDQATGKAQRIHNAGAI IEAAGKMRLGVEK LHNTHNEHLKTQLVETGRERIVDYEAFG					
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m563 . pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEK LHNTHNEHLKTQLVETGREHIVDYEAFG					
	850	860	870	880	890	900
-----						
	630	640	650	660	670	680
g563 . pep	RHELLREGTQHELGW FVYNNESDHLRTPDGAH ENWHKYDY EKVTQETQV TGTAPAKI IIA					
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m563 . pep	RHELLREGTQHELGWSVYNDES DHLRTPDGA AHENWHKYDY EKVTQKTQV TGTAPAKI IIS					
	910	920	930	940	950	960
-----						
	690	700	710	720	730	740

857

g563 . pep	GSDLIIDSKAVFNSDSRIIAGGQLLVQTEKDLHNEQTFGEKKVFSSENGKLHNYWRARRK
m563 . pep	GNDLTIDGKEVFNTDSQIIAGGNLIVQTEKDLHNEQTFGEKKVFSSENGKLHNYWREKHK
	970 980 990 1000 1010 1020
	750 760 770 780 790 800
g563 . pep	GHDETGHREQNYTLPEEITRDISLGSFAYESHKALSRHAPSQGTLPQSNRDNIRTAKS
m563 . pep	GRDSTGHSEQNYTLPEEITRNISLGSFAYESHKALSHAPSQGTLPQSN-----
	1030 1040 1050 1060 1070
	810 820 830 840 850 860
g563 . pep	NGISLPYTPNSFTPLPGSSLYIINPANKGYLVETDPRFANYRQWLGS DYMLGSLKLDPN
m563 . pep	-GISLPYTPNSFTPLPGSSLYIINPVNKG YLVETDPRFANYRQWLGS DYMLGSLKLDPN
	1080 1090 1100 1110 1120 1130
	870 880 890 900 910 920
g563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
m563 . pep	LHKRLGDGYEQRLINEQIAELTGHRRLDGYQNDDEEQFKALMDNGATAARSMNLSVGIAL
	1140 1150 1160 1170 1180 1190
	930 940 950 960 970 980
g563 . pep	SAEQAAQLTSDIVVLVQKEVKLPDGGTQT VLPQVYVRVKNGGIDGKGALLSGSNTQINV
m563 . pep	SAEQAAQLTSDIVVLVQKEVKLPDGGTQT VLPQVYVRVKNGGIDGKGALLSGSNTQINV
	1200 1210 1220 1230 1240 1250
	990 1000 1010 1020 1030 1040
g563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGILSAEQTLLLNA
m563 . pep	SGSLKNSGTIAGRNALIINTDTLDNIGGRIHAQSAVTATQDINNIGGMLSAEQTLLLNA
	1260 1270 1280 1290 1300 1310
	1050 1060 1070 1080 1090 1100
g563 . pep	GNNINNQSTAKSSQNAQGSSTYLDRMAGIYITGKEKGVLAAGKDINI IAGQISNQSDQ
m563 . pep	GNNINSQSTTASSQNTQGSSTYLDRMAGIYITGKEKGVLAAGKDINI IAGQISNQSEQ
	1320 1330 1340 1350 1360 1370
	1110 1120 1130 1140 1150 1160
g563 . pep	GQTRLQAGRDINLDTVQTGKYQEIHFADNHTIRGSTNEVGSSIQT KGDVTLGNNLNA
m563 . pep	GQTRLQAGRDINLDTVQTSKHQATHFDADNHVIRGSTNEVGSSIQT KGDVTLGNNLNA
	1380 1390 1400 1410 1420 1430
	1170 1180 1190 1200 1210 1220
g563 . pep	KAAEVGSAKGT LAVYAKNDITISSGIHAGQVDDASKHTGRSGGKNLVI TDKAQSHHETA
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	1440 1450 1460 1470 1480 1490
	1230 1240 1250 1260 1270 1280
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m563 . pep	QSSTFEGKQVVLQAGNDANILGSNVISDNGTQI QAGNHVRIGTTQTQSQSEYHQTQKSG
	1500 1510 1520 1530 1540 1550
	1290 1300 1310 1320 1330 1340
g563 . pep	LMSAGIGFTIGSKTNTQENQSQSNHEHTGSTVGS LKGDITIVASKHYEQTGSNVSSPEGNN

858

m563.ppep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGSLSKGDTTIVAGKHYEQIGSTVSSPEGNN	1560	1570	1580	1590	1600	1610
g563.ppep	LISTQSMDIGAAQNQLNSKTTQTYEQKGLTVGIQFARYRFGTTSDCRSTQSSKQVQGSKN	1350	1360	1370	1380	1390	1400
m563.ppep	TIYAQSIDIQAAHNKLNSNTTQTYEQKGLTVAFSSPVTDLAQQA- IAVAQSSKQVQGSKN	1620	1630	1640	1650	1660	
g563.ppep	DRVNMAAANAGWQAYQTGKGAQNLANGTTNAKQVSISITYEQQNRQTTQVQANQAQAS	1410	1420	1430	1440	1450	1460
m563.ppep	DRVNMAAANAGWQAYQTGKSAQNLANGTTNAKQVSISITYEQQNRQTTQVQANQAQAS	1670	1680	1690	1700	1710	1720
g563.ppep	QIQAGGKTTLYCRRCEQSNINITGSGVSGRAGTGLIADKQIHLQSAEQSNTERSQNKSA	1470	1480	1490	1500	1510	1520
m563.ppep	QIQAGGKTTLIATGAEEQSNINLAGSDVAGKAGTILADNDITLQSAEQSNTERGQNKSA	1730	1740	1750	1760	1770	1780
g563.ppep	GWNAGAAVSGQGGWSLGAAGGNVKGKGYGDSVTHRHSIGDKGSQTLIQSGGDTTIK	1530	1540	1550	1560	1570	1580
m563.ppep	GWNAGAAVSGQGGWSLGVTAGGNVKGKGYNGDSITHRHSIGDKGSQTLIQSGGDTTIK	1790	1800	1810	1820	1830	1840
g563.ppep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONAGAQTGVGYGFSASGDYSQSKIRADHA	1590	1600	1610	1620	1630	1640
m563.ppep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONASQAQTGVGYGFSAGGDYSQSKIRADHV	1850	1860	1870	1880	1890	1900
g563.ppep	SVTEQSGIYAGEDGYQIKVGNHTGLKGGIITSSQSAKDKGNRFSTGTLAGSDIQNYSQY	1650	1660	1670	1680	1690	1700
m563.ppep	SVTEQSGIYAGEDGYQIKVGNHTDLKGGIITSTQSAEDKGNRFQTATLTHSDIKNHSQY	1910	1920	1930	1940	1950	1960
g563.ppep	EGKSFGGLGASVAVSGKTLGQGAQNKPKDKHLTSIADKNGASSSVGYGSDSDSQSSITKSG	1710	1720	1730	1740	1750	1760
m563.ppep	KGESFGLGASASISGKTLGQGAQNKPKDKHLTSVADKNSASSSVGYGSDSDSQSSITKSG	1970	1980	1990	2000	2010	2020
g563.ppep	INTPKNIQITDEAAQIRLTGKIAAQTKADIDTNVTTDTAERHSGSLKNIQDKDRVQSELD	1770	1780	1790	1800	1810	1820
m563.ppep	INT-RNIQITDEAAQIRLTGKTAAQTKADIDTNVTTDTAERHSGSLKNTFNKEAVQSELD	2030	2040	2050	2060	2070	2080
g563.ppep	LQRTVSQDFSKNVQQTNTEINQHLDKLKADKEAAETAAAEALANGDMETAKRKAHEAQDA	1830	1840	1850	1860	1870	1880
m563.ppep	LQRTVSQDFSKNVQQAQNTNTEINQHLDKLKADKEAAETAAAEALANGDMETAKRKAHEAQDA	2090	2100	2110	2120	2130	2140
g563.ppep	AAKADNWQQGVILNMLASGLAEPTQSGAGIAAATASPDVSYAIGQHFKDLAQONANGKL	1890	1900	1910	1920	1930	1940
m563.ppep	AAKADNWQQGVILNMLASGLAAPTQSGAGIAAATASPAVSYAIGQHFKDLAQONANGKL	2150	2160	2170	2180	2190	2200

859

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAPIIGKWL YGKG DGGSLNAE					
	:        :         :         :					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWL YGKEKGS DLTAE					
	2210	2220	2230	2240	2250	2260
	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFTASDFASSFSYPINMX					
	:     :    :        :     :     :					
m563 . pep	EKETVTAITNVLGTATGA AVGNSATDA AQGSLNAQSAVENNDTVEQVKFALRHPRI AIAI					
	2270	2280	2290	2300	2310	2320
m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGVGNAFRHVLWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1  ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TCGGGGTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGCGG ATTTTAAACA
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451 CCTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
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551 CAGAAAGTCG TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG
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801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
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1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
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1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
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2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
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 2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT  
 2401 TTCGTCGTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT  
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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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251 YHSKIDAPVW QGDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWFFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVS DVPQTG LNPNPSPVPIQ IPSTATSGS STVSVSKPGS
501 NNPVSPPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLNLSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLAN TGKVSVARLN TEGQTLNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
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2151 YGSDGDSKNS TTRSGVNTHN IHITDEAGQL ARTGRTAKET EARIYTGIDT
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2551 TGSDDLPLAGA GNIRIPANGN VAKGDRIPTD ALASKGIKHK DRKDQLEKK*

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Computer analysis of this amino acid sequence gave the following results:

#### Homology with fha

m564/fha

ID FHAB\_BORPE STANDARD; PRT; 3591 AA.

AC P12255;

DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE FILAMENTOUS HEMAGGLUTININ. . . .

SCORES Init1: 190 Initn: 524 Opt: 594

Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

```

              10      20      30      40      50      60
m564 .pep  MNRTLYKVVFENKHNRCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
           || :||::||:: || : : ||:: | || : : | : : | : : ||:: :
fhab_borpe MNTNLYRLVFSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
              10      20      30      40      50

              70      80      90      100     110     119
m564 .pep  LSLLLG-SALILTSSSATAQGIVADKSAPAQQQPTILQTGNIGIPQVNIQTPTSAGVSVNQ
           :|:: :| :| : ||:: | || | || :| || :| || | :|::||| :|
fhab_borpe WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK
              60      70      80      90      100

              120     130     140     150     160     170     179
m564 .pep  YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSQNLNGYIEV
           : ||::| | :||::| : : :|| : || |::| :| : : : : : :| :|
fhab_borpe FQQFNVANPGVFENNGLTDGVSRIIGGALTKNPNLTR-QASAILAEVTDTPSPSRLAGTLEV
              110     120     130     140     150     160

```



m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDFFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDGOAALGSLAAKGELTVSAAARAATVA-EL---KSLDNIS					
		720	730	740	750	760	
m564	.pep	820	830	840	850	860	870
		IKGRLLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINSDDL					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETTEGSTKAGAIARLRLDI-GAKEIHN					
fhab_borpe		--GSDGAI SVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGIFAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQNINNHEKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGLHVVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGQKDQTATFHLKNGSRIEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGEHLDLGTLAAVGAVDV---NGTGDVRVAKLVSDAGADLQAGRS					
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASQGNWLNKDSRIVVGGRIITDDLNQKE					
fhab_borpe		MTLGIVDTTGDQLQARAQQKLELGSVKSDGGLQAAAGGALSAAAEVAGALELS---GQGV					
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRTDVAGTQWDSVTKKGWY---SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
		1040	1050	1060	1070		1080
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQNAASPSFQPAASAIKLIDGVSTA AVNGQRIHTGNVVSINNATVTLPNSSLYT					
fhab_borpe		SVVVRAQGNVTVGRGDPHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQLDTNHLHKRLG DGYEYQKLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKFL--NGTLRAVNDN--NETMSGRQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFLGTPG-IALSAEQVARLTS DIVWMENQTV					
fhab_borpe		VDGRPQI-----TDAVTGEARKDES VSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

[illegible]

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGEQGGSTTHRHTHVGGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGIGG-----DVDNRSV-					
		1870	1880	1890	1900		

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
		:::	:	:	:	:
fhab_borpe		VRTVSAMEYFKTLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNH--RYEGRSFGIGGS					
		::::	:	:	:	:	:
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGSDDSKNSTTRSGVNTNHIHITDEAG				
			:	:	:	:
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRVRVDQLG-----QRYGKALGMDAETKEVDGIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKEATEARIYTGITDETADQHSGLKNSFDKDAVAKEINLQREVTFEGRNAA					
		:	:	:	:	:	:
fhab_borpe		EFAADLRVTYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRV--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
			:	:	:	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYDTWKEGGIGRSILHGAAGGLTGTSLGGILAGGGSLSAAPYLDKAAENLGPAGK					
			:	:	:	:	:
fhab_borpe		AQNRGRPEGLKIGAHSAVSFSGFDALRDVGLEKRLDIDDALA AVLNVNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accgcgcgct tccaatactt
101 ccctgcggtt cgcacgcgcg aacgacaccg gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaatatacctc
201 tttgggcgaa gacgcgtccg accgtctgcc cgccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```

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```

251 TCAGCACATG GTCGGA CTGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTT AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||
g565          MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDL LMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||||
g565          AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51 CGTAACCACC ACCATTTTCG CCCGTCCAG ACCGGCGGCT TCCAATACTT
101 CCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCG GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGA CTGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCGC CGACCGAATG TTTCATTTT AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||

```

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```

a565      MDSTLSKTCVSCILLSVTTFIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
           70      80      90      100     110     120
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           |||
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
           130     140     150     160     170     180
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
           190     200     210
m565.pep  KAMANTTSAFNTSSIANSTICRQPPINAX
           |||
a565      KAMANTTSAFNTSSIANSTICRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct ttccagacgg cattttgtat gggggttaac
51  ggttggtcag cccgagtagc tcctgcatac cgtacaaacc cgttttgccg
101 ttaccctaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggctttg tgggtgattt ccacgcgttc gccgtcggtg gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcggcggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAERAG DDFAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGCCG
101 TTGACCAAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGCTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||

```

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```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51 GGTGTGTTTCTG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTACCCTG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCGC GCGGCAAAGG TCATGCGGCT
151 GCTTGCCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CCGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGCCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGCG GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq..
1  atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcggtt
51  tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtacgcag
101  caaagagggc ggatacggcg tgttggtgac gaacgcgcgc gcttgccggc
151  gcggaatcgc agctggtgca ggaaatcgcc cggaagtgc gttgaaaaa
201  cgcgctcaag gcagtggcgg aagattacga cttatcctg atcgactgtc
251  cgccttcgct gacgctgttg acgcttaacg gcttggtggc ggcgggcggc
301  gtgattgtgc cgatgttgtg cgaatattac gcgctggaag ggatttccga
351  tttgattgcg accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
401  acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctggtt
451  gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgcttttga
501  aaccgccatc ccgcgcaata tccgccttgc ggaagcgccg agccacggta
551  tgccggtgat ggcttacgac gcgcaggcaa agggtgccaa ggcgtatcctt
601  gccttgccgg acgaactggc ggcgagggtg tcggggaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAASTR RVCSPAFIRS YWAMRTCSRR RYAAKRADTA CWVRTRALAG
51  AEIELVQEIA REVRLKNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN POLDITGIVR TMYDSRSRLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GCGGGATACG
251 CTGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCGGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTGTATTG CGACCGTGCG
501 CAAATCCGT CAGGCGGTCA ATCCCGATTG GGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTCGGGGA TTTGCTTTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCCT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAEEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m567/g567 98.2% identity in 168 aa overlap

	60	70	80	90	100	110	119
m567.pep	GVYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAEEED						
g567	AFIRSYWAMRTCSRYYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAEEED						
	20	30	40	50	60	70	
m567.pep	120	130	140	150	160	170	179
	YDFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI						
g567	YDFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI						
	80	90	100	110	120	130	
m567.pep	180	190	200	210	220	230	239
	TGIVRTMYDSRRLVAEVSEQLRSHFGDLLFETVIPRNLAEAPSHGMPVMAYDAQAKG						
g567	TGIVRTMYDSRRLVAEVSEQLRSHFGDLLFETAIPRNLAEAPSHGMPVMAYDAQAKG						
	140	150	160	170	180	190	
m567.pep	240	250					
	TKAYLALADELAARVSGKX						
g567	AKAYLALADELAARVSGKX						
	200	210					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GCGGGATACG
```

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251 GCGTGTGGG TCGAACC GCCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TCGGAATATT AC GCGCTGGA AGGGATTCC GATTGATTG CGACCGTGCG
501 CAAATCCGT CAGGCGGTCA ATCCCGATT GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGCGGAGGG TGTGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYVGLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

              10      20      30      40      50      60
m567.pep      MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              |||||
a567           MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90      100     110     120
m567.pep      VYQVLLGDADVQSAAVRSKEGGYAVLGNR ALAGAEIELVQEIAREVRLKNALKAVEEDY
              |||||
a567           VYQVLLGDADVQSAAVRSKEGGYAVLGNR ALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90      100     110     120

              130     140     150     160     170     180
m567.pep      DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              |||||
a567           DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep      GIVRTMYDSR SRLVAEVSEQLRSHFGDLLETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
              |||||
a567           GIVRTMYDSR SRLVAEVSEQLRSHFGDLLETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
              190     200     210     220     230     240

              250
m567.pep      KAYLALADELAARVSGKX
              |||||
a567           KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
51 gataccttgc agaattctgc gattaaagcg ttcgcggctg cccaatattt
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaca gcccatcag gaacgaaact tcgtcttcgg ggcgacgcca
201 gttttcgggt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

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401 tgctgctctt catatctgcc ttctcgcggtt cggcggtcaa atgccgtctg  
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep  
1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL  
151 NAAP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq  
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC  
51 GATGCCTTGC AGAATCTGCC GGTGAAGCG TTCCGGCTG CCCAATATCT  
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC  
151 TGTAAAAACA GCGCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCGCA  
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG  
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC  
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT  
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG  
401 TGCTGCTTTT CATGTCTGCC TTTCCGGTTC CCGCATTCAT ATGCCGCTCTG  
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG  
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCCGTCAG TTTTGAACC  
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTCTT TGTCTTTGAG  
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA  
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG  
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC  
751 TGCCGGGTTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..  
1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL  
151 NAEPCLRNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE  
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS  
251 CRVQSQV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLRNCHQIFFFGSQEFVGFVGNVFGQ					
g568	MCLGMAVCSKMVCVLLFISAFRGSFAFKCRLNAAPX					
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDENQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1   ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTAAAAACA GCCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTTCGGTTC CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGACGGTT AAATGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 CAGTCTTCGC CGCAGCTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1   MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFDVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

m568.pep	10	20	30	40	50	60
	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	70	80	90	100	110	120
	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	130	140	150	160	170	180
	ICLGMVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	190	200	210	220	230	240
	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	250					
	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1   atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttgggtttgg tatgtgttt
251 tggcattttg gctcgccggt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCCTT TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGCTTT TCGGCGTGGT
201 TGCTATGCGG GCGGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGTTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCCGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGCGCG CGCGTTTGGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
601 TTCGATACCG TGTAAATCGG TTTGGTGCTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAGAGTGCT GCCCGGACAC GCGGCGGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRPKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAIAPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSKILPGH GGVFDRDTSI
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPDALPLAVMGLVWVADICAYFSGKAFGKHKIAPAIAPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCCTT TGGGAATATG CCCGTATGGG CGGTTTGTGC

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875

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151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCEA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGCGCGTGT TCGACCGEAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALLIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVSVSCGDL ESWLKRAAGI KDSSNLLPGH GGVFDRDTS
251 IAVISVYAAM MSVLN*

m569/a569 99.6% identity in 265 aa overlap

10 20 30 40 50 60
m569.pep MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLIALWEYARMGGLCKIKTNHYLAA
|||||
a569 MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALLIALWEYARMGGLCKIKTNHYLAA
10 20 30 40 50 60

70 80 90 100 110 120
m569.pep TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
|||||
a569 TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
70 80 90 100 110 120

130 140 150 160 170 180
m569.pep ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC
|||||
a569 ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC
130 140 150 160 170 180

190 200 210 220 230 240
m569.pep VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVSCGDLLESWLKRAAGIKDSSKLLPGH
|||||
a569 VAVYMTAVRSAGWLAFTDGTWFDTVLIGLVLTVSVSCGDLLESWLKRAAGIKDSSNLLPGH
190 200 210 220 230 240

250 260
m569.pep GGVFDRDTSIAVISVYAAMMSVLNX
|||||
a569 GGVFDRDTSIAVISVYAAMMSVLNX
250 260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

```

g570.seq..
1 atgatccgtt tgacccgcgc gtttgccgcc gccctgatcg gtttatgctg
51 caccacagcg gcgcacgcgc acaccttcca aaaaatcgcg tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttgaaa ggcagctcgc cggcgcaaaa cttaaggacg
251 caaaaaagcg gcaagccgaa gaaaaatggc gcgggctggt cgaagcgctc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgcaaa ccgcgtcatc gtcaaaatcg

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876

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401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
451 acccaatacgc acgttaccga cagcgtcatt aaagaaatga acgcccgcgtg
501 a

```

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

```

1 MTRLTRFAAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDVSI KEMNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

```

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
51 CACCGCAGGC GCGCAGCGCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
501 A

```

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

```

1 MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYN
151 TQYDVTDVSI KEMNAR*

```

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRFAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDVSIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDVSIKEMNARX					
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDVSIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDVSIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

```

1 ATGACCCGTT TGACCCGCGC GTTGGCCGCG GCTCTGATCG GTTGTGCTG
51 CACCGCAGGC GCGCAGCGCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

```

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```
a570.pep
1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
51 LDSEFSAROD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*
```

m570/a570 97.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
a570	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
a570	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX					
a570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```
g571.seq (partial)
1  atgcgcgttt tccgagtaaa ccgatttgtt gttaccgttt tggcgggcgg
51  tataggttct gccgtccac acgctgcctg cgtcggcaaa caggctcagg
101 cggacggtgc gtgcgtcttt cgcaccgggc atcggaaga gcagctcggc
151 ggagacgttg gctttttgtg tgcgcgctga gctgatttt tgcgcgtatt
201 cgtcatacac ttccgggccc agcgtgccgc ttctgtagcc gcgcaccgaa
251 cccaggccgc cgccgtagaa gttttcaaa aaggggattt ctttggttct
301 gccgtagccc cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351 ttttgc...
```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```
g571.pep (partial)
1  MRVFRVNRV VTVFGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
51  GDVGFFVAHV ADFFAVFVIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
101 AVAARNADFA AEHQREGFA...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```
m571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCGCG CCGGTGCGCG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCGCGCG TAGAAGTTTT CAAAGAAGGG
301 GATTTCITTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGCCCA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```
m571.pep
1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAADVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDGFGV
151 HARQVAARRP *
```



878

m571/g571 93.1% identity in 102 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      MRVFRVNRVVTTFGGGIGSAVPHAACVKGQAQADGACVFRGTGHREEQLGGDVGF
           10      20      30      40      50

      70      80      90     100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           60      70      80      90     100     110

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQDGFVHARQVAARRPX
           ||||
g571      EGFA
           119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCGG CCGGTCGCGG
51  AACTGCTGTT GTCGTCTAG GTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGC TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTCG GACCGAGCGT GCCGCTTCG
251 TATCCGCGCA CCGAACCAG GCCGCCGCG TAGAAGTTT CAAAGAAGG
301 GATTCTTTG GTTCTGCCG AGCCGCCCG AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGTTTTG CTTAAGGGA AGAACCAGT TTGTTGTGG
401 GTGGCGGAGT AGTATTGAG TTTGCTGCC GGCAGGCGA TTTCGGCGTT
451 CACGCCGTC AGGTAGCCG GCGTCGGCA TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1712; ORF 571.a&gt;:

```

a571.pep
1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQDGFV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      MGIAGAVNVLNPAAGRGTAVVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           10      20      30      40      50      60

      70      80      90     100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           70      80      90     100     110     120

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQDGFVHARQVAARRPX
           ||||
a571      EGFAQGEEPLVVGGGVVLQFAARQDGFVHARQVAARRPX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

1	atgtgcgcga	tctgtcggggc	ggcgggggctg	ccttcgcgcg	tcgcagcggc
51	gcaaaaaggc	aaaaccattt	atctggcaaa	caaagaaacg	ctgggtggttg
101	ccgggcgctt	ggtttatgaa	accgcccgcg	caaacggcgc	ggcgatgtttg
151	cccgctgcga	gcgaacacaa	cgcatttttc	caagttttgc	gcggcgattat
201	cacagaccgt	ctgaacgaac	acgggcatcga	ttcgattatc	ctgaccgctt
251	ccgggcggcc	gtttttaaca	accgatttaa	gcactgtcga	cagcattacg
301	cccgagcagg	cggctcaaca	ccccaattgt	cgtatggggc	gcgaaatctg
351	cgtcgattca	gcgcatatgg	caacaagggg	cttggaaact	gttaagcgcg
401	attggtcgtt	caactgtccg	cccgacaaac	tcgaagtctg	catccatccc
451	caatccgtga	tacacagtat	gggtgcgtac	cgcgacggct	ccgtgtcggc
501	gcaactggcg	aatcccgcat	tgcgaacgcc	catcgctatt	tgtttggcgt
551	tgcccgagcg	catcgattcg	gggtgcggca	aaatcgattt	cggcgcatctg
601	tccgcgctga	ccttccaaaa	gcccgcatct	ggcgcgtctc	ccttcgtgaa
651	gttcgcttat	gaaacataaa	acgcaggcgg	agccgcgcc	tgcgtattga
701	acggcgccaa	cgaaacatgc	tgcgcgcctt	tttggacggy	acagattaa
751	ttatccgcga	ttgcgaaaa	cgtcgcccat	tgtcttcgac	aaactatttc
801	aaacggcatg	gggcatatag	aaggactgtt	ggcgcaagat	gcccggcac
851	qccgcacaagc	gcggcgatct	atcggcacac	tcgccttga	

g572.pap..

1	MCAIVGAAGL	PSALAAQKG	KTIYLANKET	LUVSGALFME	TARANGAAVL
51	PVDSEHNATF	QVLPRDYTR	LNEHGIDSII	LTASGGFFLT	TDLSTFDSIT
101	PEQAVKHPNV	RMGRKISVDS	ATMMARKTGLE	IEAHWLFERNP	PKDLGVVTHP
151	QSVIHSMPWY	RDGSLVALQG	NPDMRTPIAL	CLGLPERNCIS	GVGKLDLFGAL
201	SALTFOKPDF	GRFPCLFKAY	ETINAGGAAP	CVLNAANETA	VAAFLDGOIK

m572.seq..

1	ATGTGCGCCA	TCGTGCGGGC	GGTGGGGCTG	CCTTCCGCGC	TCGCAGCGGC
51	GCAAAAAGCG	AAAAACCATTT	ATCTGGCAAA	CRAAGAAACG	CTGGTGGTTT
101	CCGGCGCGTT	GTTTATTGAA	ACCGCCCGTG	CAACCGCGCG	GGCAGTGCAT
151	CCCTGCGACA	CGGAACACAA	CCCGTTTTC	TTAGTTTTCG	CGCGCGGATT
201	CGCGGCGCGT	CTGAACGAAC	ACGGCATCGC	TTCGATTATC	CTGACCGCTT
251	CGCGGCGGCC	GTTTCTGCC	GACCATTTA	ACACGCTTCA	CGCATTTACG
301	CCCGCCCAAG	CGCTCAACA	CCCAATTGG	CGTATGGGAC	GCAAAATCTC
351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGT
401	ATTGGCTGT	CAACTGTCG	CCCGACAAC	TCGAAGTCGT	CATCCATCCG
451	CAATCCGTGA	TACACAGCAT	GGTGCCTAC	CGCGACGGCT	CCGTGCTGGC
501	GCAACTGGGG	AATCCCGATA	TGCGAACGCC	CATCGCTTAT	TTGTTGGGTT
551	TGCCCGAGCG	CATCGATTCT	GGTGTGCGCG	ACCTGGATT	CGACGCATTG
601	TCGCGCTGA	CCTTCCAAAA	GCCGCACATT	GACCGCTTCC	CCTGCTGTAG
651	GCTGCGCTAT	GAAGCGATGA	ACGCAGGCGC	AGCCGCGCTC	TGCGTATTGA
701	AGCGCGCCAA	CGAAGCGCGC	GTGCGCGCCT	TTTGTGACGG	ACAGATTAA
751	TTTACCGACA	TGCGCAAAAC	CGTGCGCCAC	TGCTTCAAGT	AAGACTTTTC
801	AGACGGCATA	GGGCATATAG	GGGGGCTCTT	GGCGCAAGAT	GCCCGGACAC
851	GGCGACAAGC	GCGAGCATTT	ATTGGGCATA	TCGCGTGA	

m572.per..

1	MCAIVGAVGL	PSALAAQKG	KTIYLANKET	LUVSGALFME	TARANGAAVL
51	PVDSEHNAV	QLPRDYAGR	LNEHGASII	LEAGSGPFLT	ADLNTFDTRT
101	PAQVAKHPNW	RMKRISVDS	AMTNMKGLE	IEAHWLFENC	PDKLVVHHIP
151	QSVIHSVMRY	RDGSVLAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDLDFDAL
201	SALTTPQKPDF	DRFPCLLRLA	EAMNAGGAAP	CVLNAANAEA	VAAFLDQGQTK
251	FTDIATKVAH	CLAQGSDGI	GDIGGLAOD	ARTRAAORAE	IGTLR*

m572/g572 92.9% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAAGLPSALAAAKGKTIYLANKETLVVSGALFMETARANGAAVL	PVDSEHNAVF				
g572	MCAIVGAAGLPSALAAAKGKTIYLANKETLVVSGALFMETARANGAAVL	PVDSEHNAIF				
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLNEHGIDSIILTASGGPPLTADLNTFDRITPAQAVKH	PNPWRMGRKISVDS				
g572	QVLPRDYYDRLNEHGIDSIILTASGGPPLTDLSTFDSITPEQAVKH	PNPWRMGRKISVDS				

880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFOKPDFRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGKLDGALSALTFOKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFSNMGDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572.seq
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTGC CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCGGATTTAA ACACGTTCGA CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGCTGTG CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCC GGTGTCGGCG ACCTGGATT TCGACGCATTG
601 TCCGCGCTGA CTTTCCAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCT TTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGACAAGC GCGGGCATT ATCGGCACAC TCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572.pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS VVGDLDFDAL
201 SALTFOKPDF DRFPCLLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572.pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572.pep	QVLPDYGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPDYTGR LNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1 atgccctgtt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51 gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaaatct cggcagggtc ttccgcggtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaaccgg tcggaccggt taccagcacc atcccgttag gacgggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaaccg agctggtcga
351 tgttcaaaga cggcgcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tccatccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc gggaagcaag ctgccccctt
551 accgcaatgg gcggtcgaac cacctcgcgg agctgccctt ccacacggaa
601 acggatacgc gcatttgtgt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcacccgac aaagttttat ggataaacct cggaacaggg
701 ccgtcttctg cctcctcgtc gtgatatac aggggtgtgc ttctctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgatgtcgaa cgcgaaccca
801 cccaatcgag caaacccgcc aactggatc cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcatctgggt
901 cggatcggaa accgcaaaaa atactttgtc gccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgctcctcgg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgataaac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttggcgga aatgacacgg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1 MPCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPFPGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPTAQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTACCAAC aCaw.TTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGTAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

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```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCTTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCT
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

```

m573.pep..
  1  MPCLCRNLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
 51  DARQVNLGRV FRCNIIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101  RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151  LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201  TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLF
251  LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301  RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351  RNQCRKRLGR NDTV*

m573/g573 95.9% identity in 364 aa overlap

      10      20      30      40      50      60
m573.pep  MPCLCRNLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGRV
          |||
g573      MPCLCRNLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGRV
          |||

      70      80      90     100     110     120
m573.pep  FRCNIIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXFFLKRKTELVDVQR
          |||
g573      FRCNIIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXFFLKRKTELVDVQR
          |||

      130     140     150     160     170     180
m573.pep  RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXGSK
          |||
g573      RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQTRHYLNPXGSK
          |||

      190     200     210     220     230     240
m573.pep  LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV
          |||
g573      LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV
          |||

      250     260     270     280     290     300
m573.pep  VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC
          |||
g573      VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC
          |||

      310     320     330     340     350     360
m573.pep  RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR
          |||
g573      RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR
          |||

m573.pep  NDTVX
          |||
g573      NDTVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq  
1 ATGCCCTGTT TGTGCCGCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC  
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC  
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT  
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA  
201 CCGACTCCGT ATTCAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA  
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT  
301 CGCTTCCAAC AACATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA  
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG  
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC  
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG  
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGGAAGCAAG CTGCCCCCTT  
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA  
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC  
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG  
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTCTCTCTC  
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA  
801 CCAAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA  
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT  
901 CGGATCGGAA ACCGCAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA  
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC  
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCCT  
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep  
1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI  
51 DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN  
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA  
151 LLKGQLHPAV LRYPFNGVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE  
201 TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE  
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC  
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP  
351 RNQCRKRLGR NDTV\*  
  
m573/a573 98.6% identity in 364 aa overlap  
  
m573.pep 10 20 30 40 50 60  
MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV  
|||||  
a573 MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI DARQVNLGRV  
10 20 30 40 50 60  
  
m573.pep 70 80 90 100 110 120  
FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHFFLKR LKTELVDVQR  
|||||:|||||  
a573 FRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRFQQQFFLKR LKTELVDVQR  
70 80 90 100 110 120  
  
m573.pep 130 140 150 160 170 180  
RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFNGVQTRHYLNPGSK  
|||||  
a573 RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFNGVQTRHYLNPGSK  
130 140 150 160 170 180  
  
m573.pep 190 200 210 220 230 240  
LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV  
|||||  
a573 LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRAVFCLLV  
190 200 210 220 230 240  
  
m573.pep 250 260 270 280 290 300  
VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC  
|||||  
a573 VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC  
250 260 270 280 290 300

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	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360

m573.pep	NDTVX
a573	NDTVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1 atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51 attgtggatt atcctgtctg cgattatcct ttgtcccgtc ttcttcacga
101 tgggctgggt tgccgcccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc ctccgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caacagcggg cgccgcccga gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaaag cgccgggtttg gtccgatcgt ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgcccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagcctatg ccgccatcga gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg cttaaaggcg agaaagaagc
951 cgccgcaaac gccgtcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gctcgggttg aaactcagcg atttgatcc ggttggaaa
1051 gccgatgccg acatgatgcg ttcggttatc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1 MLPLNLSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTIGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGMAREAR QHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAAALFVS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFFAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1 ATGCGCCGGA ATCTACCAAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51 ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCCGC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCAGAAAACG ACAAAGCCAT CAACATACAC CCGACAATGC TCGATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTCGGGG
451 CTGCAAGACG GTAAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACCTTGCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGGTTT

```

m574.pcp..

```

1      MRPNLPNSLK  KADMONElWI  ILLPIILLPV  FFAMGWFAAR  VDMKTVLKQA
51     KSIPSGFYK  LDALVDRNSG  RAARELAEV  DGRPPSYADL  L7LGLKLYRQ
101    GENDKAINIH  TRMLDSPTVS  GEKRAVLVF  LAQNYQSAGL  VDRASQIFLG
151    LQDGKMAREA  RQHLLNIYQQ  DRDWEKAVET  ARLLSHDDQT  YQFEIAQFYC
201    ELAQAALFNS  RFDVARFVNG  KALEANKCT  RANMILGDIE  HRQGNFPAAV
251    EYAAAEQON  HAYLSMVEGK  LYEAYAAQEG  PEGGINLRT  YQGTFFELDL
301    INVVYEKSL  LKCEKEAAQT  AVELVRKRPD  LNGVYRLGL  KLSDMMPAWK
351    ADADMMSVI  GRQLQRSVMY  RCRNCHFSQS  VFFWHCPACN  KWQTFPTPKI
401    EV*

```

m573/q573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574 .pep	MRPNLPNSLSKKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
g574	MLPNLPNSLSKKADMDNELWIILLPIILLPVFFTMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574 .pep	LDALVDRNSGRAARELAEEVVDGRPQSYDNLNLTLGKLYRQRGENDKAINIHRTMLDSPDTV					
g574	LDALVDRNSGRAARELAEEVVDGRPQSYDNLNLTLGKLYRQRGENDKAINIHRTMLDSPDTV					
	70	80	90	100	110	120
m574 .pep	GEKRRARVLFEFAQNYQSAGLVDRAEQIFLGLQDGMAREARQHLLNIYQQDRDWEKAVET					
g574	GEKRRARVLFEFAQNYQSAGLVDRAEQIFLGLQDGMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574 .pep	ARLLSHDDQTYQFEIAQFYCELAQAALPKSNFDFVARFNVGKALEANKKCTRANMILGDIE					
g574	AQLLSHDEQTYQFEIAQFYCELAQAALPKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574 .pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQCKPEEGLNRLTGYMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQCKPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
m574 .pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAAWKADADMMSVI					
g574	INVVYEKSLLLKGEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDLDPAAWKADADMMSVI					
	310	320	330	340	350	360
m574 .pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
g574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		
m574 .pep						
g574						



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1   ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAAGTCGT CACGCGCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GCGGAAAACG ACAAGGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTT AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCCGCC CAAGCCCGAC CTCACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCT
1151 GGCATTGTCC TGCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1   MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLSDPDTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAALEFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSLDPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHEKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

```

          10      20      30      40      50      60
m574.pep  MRPNLPNSLKKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
          |||
a574       MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
          10      20      30      40      50      60

          70      80      90     100     110     120
m574.pep  LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSDPTV
          |||
a574       LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINMHQTLSDPDTT
          70      80      90     100     110     120

          130     140     150     160     170     180
m574.pep  GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET
          |
a574       GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET
          130     140     150     160     170     180

          190     200     210     220     230     240
m574.pep  ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE
          |||
a574       ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE
```

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGYMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKGPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDINGVYRLLGLKLSOLDPAWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtcaaaca gtccgccttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcgggaaac ggtgttacgg gtttcgtcgg tcggcggtgc gatggcagaa
201 gcggcggtct cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttgacag ggggtacaggt ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcgggt cgaacggcgg gtttttcgcg
351 ttttgcttcg ggcgcggaac cttttgcttc aggtttttca accggttttt
401 cgacagggtt ctctatcggt ttctccacag ttgctgtttt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttgcgcgttt gcgggttggg
501 ttgttcggtc ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1  ..MPCLRRQAAR CTNRRTRDQT VRFRLLRQK PVRQVRQVR RQLHWLFPQQ
51  VRKRCYRFRR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGPSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDSG
151 DGMDAVSALG FAVCGLGCSA LIFLGAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq..
1  ATGCTTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCGGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCCGG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGCTGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCCGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCGCA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCCTTCGG AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCCGTGC GCGTGTGAT GGCAGAAGCG GCGGCTTCTT GGGGGGCGGA
801 TTCGGCAGCG GTTTCGGATG CGGCAGTATT TGCAGCGGGT ACAGGTTCCG
851 GTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTTGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCGGA TGTGA

```

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This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep  
 1 MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLESEK VSTVSGLFSA  
 51 VWAIDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV  
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSL DSPSKASVSF  
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR  
 201 RKSSSRAINA APPPASSKVY EPPNRPNSNP LSVSSSAETC STGSETALPV  
 251 SSVGVSMSEA AASWGADSA VSDAAVFAAG TSGRTAGFS AFASGAATFA  
 301 SGFSTGFSTV ACLDGS DGM DAVSALGFAVC GLGCSALILF RFGM\*

m575/g575 70.2% identity in 114 aa overlap

	240	250	260	270	280	
m575.pep	SSAETCSTGSETALPVSSVGVSM	AEAAASWGADSA	AVSDAAVFAAGTG	-----		
g575	LHWLFPPQVRKRCYRFRRSACRWQKRLL	GGADSA	AVSDAAVFAAGTGPGWRSVAEAGVS			
	50	60	70	80	90	100

	290	300	309	310	320	
m575.pep	-----SGRTAGFS	AFASGAATFASGFSTGFST	-----	VACLDGS	DGM DAVSALGFA	
g575	DTAGLGSGRTAGFS	AFASGAATFASGFSTGFSTGFS	IGFSTVACLDGS	DGM DAVSALGFA		
	110	120	130	140	150	160

	330	340	
m575.pep	VCGLGCSALI	-----LFRFGMX	
g575	VCGLGCSALIFL	GAALILFRFGMX	
	170	180	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq  
 1 ATGGTTTCGG GCGAGGAAGC CTTAGGAAG CCTGCCAGTC CCGAGGGTGA  
 51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG  
 101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCGGGTTT GTTTTCGGCA  
 151 GTTTGGGCGA CAGATTCCGG TCGGGCGTG TCGATGACGA TTTCGACAGG  
 201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA  
 251 TGGCGTCCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA  
 301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC  
 351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT  
 401 TTGCGGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTT  
 451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CCACTTCGGC  
 501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT  
 551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG  
 601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG  
 651 CAAGGTGTAC GAACGCCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG  
 701 AAACCTGTTT GACAGGTTTC GAAACGGCGT TACCGGTTTC GTCGGTCCGC  
 751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT  
 801 TTCCGATGCG GCAGTATTTG CAGCGGGTAC AGGTTCGGGT CGAACGGCCG  
 851 GTTTTCCCGC TTTTGCTTCG GGCGCGGCAA CTTTGTCTTC AGGTTTTTCA  
 901 ACCGGTTTCT CTACCGTTGC CTGTTTGGAC GGTTTCGGAC GCATGGATGC  
 951 GGTTCGGCT TTGGGTTTCG CCGTTTCCGG TTTGGGTTGT TCCGCTTTGA  
 1001 TCCTGTTTCA ATTCGGAATG TGA

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep  
 1 MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLESEK VSTVSGLFSA  
 51 VWAIDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV  
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSL DSPSKASVSF  
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR  
 201 RKSSSRAINA APPPASSKVY EPPNRPNSNP LSVSSSAETC STGSETALPV  
 251 VSMEEAASW GADSAVSDA AVFAAGTGSG RTAGFSAFAS GAATFASGFS  
 301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM \*

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m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
m575.pep	70	80	90	100	110	120
	SMTISTGLYGLKVGSGSYTLSVDSMAFQASARFWSSSCVSAAPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSGSYTLSVDSMAFQASARFWSSSCVSAAPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
m575.pep	130	140	150	160	170	180
	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR					
	130	140	150	160	170	180
m575.pep	190	200	210	220	230	240
	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
m575.pep	250	260	270	280	290	300
	STGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGTSGRGTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGTSGRGTAGFSAFASGAATFA					
	240	250	260	270	280	290
m575.pep	310	320	330	340		
	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacaggcgcg
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaaagaat caaatgacc gaagagcagg cccagggaat gatgatgaaa
151 ttctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaagcccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaagggcgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcgcgcg acccgaaaac
601 gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1738; ORF 576.ng&gt;:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLEKGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA

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51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGGACCGA AGCGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTGG TATTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ
g576	MGVDIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITQGE	GKQPTKDDIV
g576	EQQAKAVEKH	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITQGE	GKQPTKDDIV
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID	GTVFDSSKAN	GGPVTFPLSQ	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE
g576	TVEYEGRLID	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPN	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VNX	
g576	QGAGEKIGPN	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VNX	
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA

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601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA  
 651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG  
 701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGTATGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

a576.pep  
 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ  
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPAQVDIKK VN\*

m576/a576 99.5% identity in 222 aa overlap

m576.pep				10	20	30
				MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV
a576	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV
	30	40	50	60	70	80
m576.pep		40	50	60	70	80
		FTEAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK
a576		FTEAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK
	90	100	110	120	130	140
m576.pep		100	110	120	130	140
		KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN
a576		KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN
	150	160	170	180	190	200
m576.pep		160	170	180	190	200
		VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
a576		VILGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
	210	220	230	240	250	260
m576.pep		220				
		KQPAQVDIKK	VNX			
a576		KQPAQVDIKK	VNX			
		270				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1.seq  
 1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC  
 51 ACTTTCCGCC TGCAGCAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC  
 101 CTGCCGCCG TTTCTGCCG CAGGCGGACA CCTTTCAAT CGGCAGCACG  
 151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA  
 201 ACAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG  
 251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG  
 301 GCCCAGGAAG TGATGATGAA ATTCTTGCA GAGCAGCAGG CTAAAGCCGT  
 351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT  
 401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT  
 451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAAACAGC CGACAAAAGA  
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT  
 551 TCGACAGCAG CAAAGCCAA CCGCGGCCGG CCACCTTCCC TTTGAGCCAA  
 601 GTGATTCCGG GTTGGACCGA AGCGGTACGG CTTCTGAAAG AAGGCGGCGA  
 651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG  
 701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTGACGT GAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep  
 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ  
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPDQVDIKK VN\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq  
 1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC  
 51 ACTTTCCGCC TCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC  
 101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC  
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA  
 201 GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAAGTC TTTACCGAAG  
 251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG  
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAg GAACAACAGG CTAAGCCGT  
 351 AGAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT  
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC  
 451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA  
 501 GCACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT  
 551 TCGACAGCAG CAAAGCCAAC GCGGCGCCCG TCACCTTCCC TTTGAGCCAA  
 601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA  
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG  
 701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTGTAGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep  
 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ  
 201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPAQVDIKK VN\*

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TL	SAALALSACGKKEAAPASASEPAASAA	QGDTSSIGST	MQQASYAMGV	
m576-1	MNTIFKISAL	TL	SAALALSACGKKEAAPASASEPAASAA	QGDTSSIGST	MQQASYAMGV	
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASGLQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASGLQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGV	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGPN
m576-1	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGV	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VN		
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

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1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGAAGCCT
401 TTCTGAAGA AATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGGCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAT CGGCCCGAAC GCCACTTGG TATTGTATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

```

a576-1.pap
1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LOYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pap	MNTIFKISAL TLSAALALSACGKKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL TLSAALALSACGKKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pap	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pap	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pap	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pap	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pap	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pap	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANG GGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pap	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
	250	260	270			
a576-1.pap	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLV KIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

### Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The



hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

-- The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1   atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttatttacg gagcaaacat gaaactatc tataccgtca tcaaatcat
201 tatcctgctg ctcttctctg tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgtcgt cggcatcgtg ttcggaatgt ttgccctggt
351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1   MERSGVFGKI VGNRILRMPS EHAAAFYKP CKSFKLTQSW FRVRSCPCGV
51  FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTFSYLPG QSVNPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1   ATGGAAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAATCGT
101 TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCTCTG TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCTTA CCTGCCGGGG CAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTGTAGT CCGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1   MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGCV
51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPG QKFDLPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERNGVFGKIVGNRILRMSS	EHAAASYPKPKCSFKLAQSW	FRVRSC	LG	GV	FIYGANMKLI
g577	MERSGVFGKIVGNRILRMP	SEHAAAFYPKPKCSFKLTQSW	FRVRSC	PC	GV	FIYGANMKLI
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIILL	LFLLLAVINT	DAVTFSYLPG	QKFDLPLIVV	LFGAFVVGII	FGMFALFGRL

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```

|||||
g577 YTVIKIIILLFLLLAVINMDAVTFSYLPGQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577.pep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
|||||
g577 LSLRGENSRRLRAEVKKKSARLSGQKLTAPPIQNAESAQKFX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1 ATGGAAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
51 TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAAACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CGTTTGCTGT CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1 MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSEKLAQSW FRVRSCPGGV
51 FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPG QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENGR LRAEVKKNAR LTKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.pep MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCLGGVFIYGANMKLI
|||||
a577 MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSEKLAQSWFRVRSCPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577.pep YTVIKIIILLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
|||||
a577 YTVIKIIILLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577.pep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
|||||
a577 LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQFX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1 atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51 cgcgccacag ttcggtgggt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aagggccagt gggcgatgag
151 ggcgatttcg ctttcgctgt atttcattgt gtttagacct tcggtttcgc
201 cgttttccaa aacacggatg ccgcgcggtt cgccgaaata aatatcgccg
251 gtaagttcgc gcacaatcaa aatatccaaa ccggcaacga tttcaggctt
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1 MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGDA
51 ADFAFAVFGH VVAFVFAVFQ NTDAARFAEI NIAGKFAHNQ NIQTGNDFRL

```

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101 ERGGVG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTCG TCGTTTTTGG GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT

```

-- This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDPRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQ	FGGFQNVGFAYGTDFFAAFL	GGLEGNMGNTADFAFAVFHG			
		:			:	
g578	MGKLDIGILFADFFKDFAPQ	FGGFQNVGFAYGADFFAAFL	GGLEGHVGDADFAFAVFHG			
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQ	NADAARFAEIDVAGEFAHNQ	NIQTGNDPRL	QRGGVGX
		:		
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQ	NIQTGNDPRL	ERGGVGX	
	70	80	90	100

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTCG TCGTTTTTGG GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGN
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDPRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQ	FGGFQNVGFAYGTDFFAAFL	GGLEGNMGNTADFAFAVFHG			
		:			:	
a578	MGKLDIRVFFADFFKDFAPQ	FGGFQNVGFAYGADFFAAFL	GGLEGDVGNADFAFAVFHG			
	10	20	30	40	50	60

	70	80	90	100
m578.pep	VVAFAFAVFQ	NADAARFAEIDVAGEFAHNQ	NIQTGNDPRL	QRGGVGX
		:		
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQ	NIQTRNDPRL	ERGGVGX	
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```

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```

51   TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101  CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151  GGGCGGGGTT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201  TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAA GTCGGCGACT
251  TTATCCGTGT CGGCGGTTT GAAGGATATG TCCGGGAAAT CAAATGGTG
301  CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351  CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTGCC
401  GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451  AAAGAGGCGG TGTGAAAGC CGCCGCCGAA CACCCTTGA GCGTTCAAAA
501  CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGG GACAATGCCA
551  TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601  CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGA AAGTCAATAT
651  CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGGCGGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCCGTTCAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGG GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG  CGATGACGCG  CGCGCAGGTC  GATGCCACGC  TGATTAGTTT
51  TTTGTGTAAT  GTTGCCAATA  TCGGGCTATT  GATTTTGGTG  ATTATTGCCG
101  CATTGGGCAG  ATTGGGCGTT  TCCACAACAT  CCGTAACCGC  CTTAATCGGC
151  GGCGCGGGTT  TGGCGGTGGC  GTTGTCTTGT  AAAGACCAGC  TGTCCAATTT
201  TGCCGCCGGC  GCGCTGATTA  TCCTGTTCCG  CCCGTTCAAA  GTCGGCGATT
251  TTATCCGCGT  CGGCGGTTTT  GAAGGATATG  TCCGAGAGAT  TAAATGGTG
301  CAGACTTCTT  TCGGACGAC  CGACAACGAA  GAAGTCGTGC  TGCCCAACAG
351  CGTGGTGATG  GGCAACAGCA  TCGTCAACCG  TTCCACACTG  CCGCTGTGCC
401  GCGCCCAAGT  GATAGTCGGC  GTCGATTACA  ACTGCGATT  GAAAGTGGCG
451  AAAGAGCGCG  TGTGAAAGC  CGCCGTCGAA  CACCCTTGA  GCGTTCAAAA
501  CGAAGAGCGG  CAGGCCGCG  CCTACATCAC  CGCCTGGGC  GACAATGCCA
551  TCGAAATCAC  ATTATGGGCT  TGGGCAAACG  AAGCAGACCG  CTGGACGCTG
601  CAATGCGACT  TGAACGAACA  AGTGGTCGAA  AACCTCCGCA  AAGTCAATAT
651  CAACATCCCG  TTCCCGCAAC  GCGACATACA  CATCATCAAT  TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV  DATLISFLCN  VANIGLLILV  IIAALGRLGV  STTSVTALIG
51  GAGLAVALSL  KDQLSNFAAG  ALIILFRPFK  VGDFIRVGGF  EGYVREIKMV
101  QTSRLTTDNE  EVVLPNSVVM  GNSIVNRSTL  PLCRAQVIVG  VDYNCDLKVA
151  KEAVLKAAVE  HPLSVQNEER  QAAAYITALG  DNAIEITLWA  WANEADRWTL
201  QCDLNEQVVE  NLRKVNINIP  FPQORDIHIIN  S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

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```

1  ATGGACTTCA  AACAAATTGA  TTTTTCACAC  CTGATCAGTG  TTTCCGGTTG
51  GGGGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTCTTGGTC  GGGAAATGGG  CGGCGAAACG  CATTGTCGCC
151 GTAATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTTGG  ACGGTTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGCGCGCGG  GTTGGCGGT  GCGTGTGTC  TTAAGAGACC  AGCTGTCCAA
351 TTTTGGCGCC  GCGCGCTGA  TTATCCTGTT  CCGCCCGTTC  AAAGTCGGCG
401 ACTTTATCCG  TGTCGGCGGT  TTTGAAGGAT  ATGTCCGGGA  AATCAAAATG
451 GTGCAGACTT  CTTGCGGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCAGC  CTGCCGCTTT
551 GCGCGCCCCA  AGTGATAGTC  GCGCTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGTC  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGCCCG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH  LISVSGWHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLTTDN  EEVLPNSVV  MGNSIVNRSS  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAA  EHPLSVQNEE  RQPAAYITAL  GDNAIEITLW  AWANEADRWT
251 LQCDLNEQVV  ENLRKVNINI  PFPQDIHII  NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA  AACAAATTGA  TTTTTCACAC  CTGATCAGTG  TTTCCGGTTG
51  GGAGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTTTCGGTC  GGGAAATGGG  CGGCGAAACG  CATTGTCGCT
151 GTGATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTTGG  CAGATTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGCGCGCGG  GTTGGCGGT  GCGTGTGTC  CTGAAAGACC  AGCTGTCCAA
351 TTTTGGCGCC  GCGCGACTGA  TTATCCTGTT  CCGCCCGTTC  AAAGTCGGCG
401 ATTTTATCCG  CGTCGGCGGT  TTTGAAGGAT  ATGTCCGAGA  GATTAAGATG
451 GTGCAGACTT  CTTGCGGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCACA  CTGCCGCTGT
551 GCGCGCCCCA  AGTGATAGTC  GCGCTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGTC  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGGCTG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH  LISVSGWEHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLTTDN  EEVLPNSVV  MGNSIVNRST  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAV  EHPLSVQNEE  RQAAAYITAL  GDNAIEITLW  AWANEADRWT
251 LQCDLNEQVV  ENLRKVNINI  PFPQDIHII  NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
	10	20	30	40	50	60
m579-1.pep	VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVLPNSVVMGNSIVNRST					
	130	140	150	160	170	180

900

```

|||||
g579-1      G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V V L P N S V V M G N S I V N R S S
              130      140      150      160      170      180

              190      200      210      220      230      240
m579-1.pep  L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W
              |||||
g579-1      L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A E H P L S V Q N E E R Q P A A Y I T A L G D N A I E I T L W
              190      200      210      220      230      240

              250      260      270      280
m579-1.pep  A W A N E A D R W T L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S X
              |||||
g579-1      A W A N E A D R W T L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S X
              250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAATTTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGGTTC GGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTGATGAGGG CGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GCGCGCGCGG GTTGGCGGGT GCGGTGTCC TTGAAAGACC AGCTGTCCAA
351 TTTTGGCGCC GCGCGCGTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGCGGGT TTTGAAGGAT ATGTCCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACCCCTT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCTACAT CACCGCCTTG GGCGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACGCGACAT ACATCATC AATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  M D F K Q D F L H L I S A S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A
51  V M R A A M T R A Q V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I
101 G G A G L A V A L S L K D Q L S N F A A G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M
151 V Q T S L R T T D N E E V V L P N S V V M G N S I V N R S T L P L C R A Q V I V G V D Y N C D L K V
201 A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W A W A N E A D R W T
251 L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S *

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

              10      20      30      40      50      60
a579-1.pep  M D F K Q D F L H L I S A S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q
              |||||
m579-1      M D F K Q D F L H L I S V S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q
              10      20      30      40      50      60

              70      80      90      100     110     120
a579-1.pep  V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A
              |||||
m579-1      V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A
              70      80      90      100     110     120

              130     140     150     160     170     180
a579-1.pep  G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V V L P N S V V M G N S I V N R S T
              |||||
m579-1      G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V V L P N S V V M G N S I V N R S T
              130     140     150     160     170     180

              190     200     210     220     230     240
a579-1.pep  L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W
              |||||
m579-1      L P L C R A Q V I V G V D Y N C D L K V A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W
              190     200     210     220     230     240

              250     260     270     280
a579-1.pep  A W A N E A D R W T L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S X

```

901

|||||  
m579-1      AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX  
                 250            260            270            280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq  
1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc  
51 cgcgtcgcag cccatttcga tggcaaggca gacttcgccg atcatgtcgc  
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca  
151 tcgaaaatca gcttggtaaa gccgttgctc caaccgttgg caatcgcacg  
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg  
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg  
301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..  
1 MDSPKVGCGW MVLPMASASQ PISMARTSP IMSPPFGPTM PPPMMRPVSA  
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV  
101 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..  
1 ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC  
51 CGCGTCGCAG CCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC  
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA  
151 TCAAAAATCA GCTTGGTAAA GCCGTGTCG CAACCGTTGG CAATCGCACG  
201 GCCGGAAGCC GCCACGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG  
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG  
301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..  
1 MDSPKVGCGW MVLPMASASQ PISMARTSP IISPPFGPTM PPPMMRPVSA  
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV  
101 \*

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
g580	MDSPKVGCGWMVLPMASASQPISMARTSPIMSPPFGPTMPPPMRPVSASKISLVKPLS					
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
	70	80	90	100		
g580	QPLAIARPEAAHGKLALVILRPDALADNSVSPHATSGEVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq  
1 ATGGATTTCG CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC  
51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG  
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA  
151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG  
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG  
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG  
301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep  
1 MDSPKVGCGW MVLPMASASQ PISMARTSP IMSPPFGPTM PPPMMRPVSA  
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV



902

101 \*

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQFISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	:     :     :     :     :					
a580	MDSPKVGCGWMVLPMSAASQFISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
	:     :     :     :     :					
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..  
 1 atgcacttcg cccagcttgt gggctcaaacc ggtatagaac aaaatacgtt  
 51 ctgtcgtcgt ggttttacc gcacgatgat gggcggaat accgatgttg  
 101 cgggtacaggc tgatcggggt cttacgagcc attttattag cctttcaaaa  
 151 ttagaaacgg aagtgagaga atgcttgggt ggcttcagcc atacgggtga  
 201 cttcttcacg ttttttcaac gcaccgccac ggccttcgga cgcacaaac  
 251 aactcgctg ccaaacgcag atccatggat ttctcaccac gtttcggggc  
 301 cgcgtcgca acccaacgca ttgccaagc cagacggcgt ga

This corresponds to the amino acid sequence &lt;SEQ ID 1780; ORF 581.ng&gt;:

g581.pep..  
 1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LSHFISLSK  
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG  
 101 RVANPTHQCS QTA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..  
 1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT  
 51 CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA  
 101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA  
 151 TTAGAAACGG AAGTGAGAGA ATGCTTGTGTT GGCTTCAGCC ATACGGTGTA  
 201 CTCTTCACG TTTTTCACAC GCACCGCCAC GGCCTTCGGA CGCATCAATC  
 251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC  
 301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

This corresponds to the amino acid sequence &lt;SEQ ID 1782; ORF 581&gt;:

m581.pep..  
 1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LSHFISLSK  
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGLTTFAG  
 101 RIANPAHCQS QTA\*

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRG LSHFISLSKLETEVRECFV					
	:     :     :     :     :					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRG LSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGLTTFAGRIANPAHCQSQTAX					
	:     :     :     :     :					
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHQCSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
  1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTGTGT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRG	LTSHFISLSKLETEVRECFV				
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVQADRG	LTSHFISLSKLETEVRECFV				
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX				
a581	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX				
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatgtt acgcttttgg
101 cgtgttacga caggattttt gggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttgatg aaggggcagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttcctgc cgacagtgcg ggcgaacccg ccgatattcta tacgccttgc
301 agcttgatgc acgacttggc caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaacgtgc ggaacccaaa ttgcagggtt cgttcaaaag
501 caaaattgcc gaaaatttgc ttaaaacccg ccgggatctg tggttcggct
551 acacccaaag atccgatagg cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa attttcctga ccagccctgt
651 gaagggcagg ttgcccgttc gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgct ccgaatcgcg ttcgtggaac
751 aggtatttat ccatggcagg catggaatgg ggcgaattga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatatggc acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacgggt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
 51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPPFW NNSPNYAPSS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIDYIM GYGDVKLQYR
301 LNDQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGCTTTC GGCAGGCGAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAA GCGGGGATG
251 CGCTTCTGTC CGACAGTGC GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTTAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCGA ATACGGATTA CAAACCTGAA ATTTTCTGTA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CGCGGATAAA AACGACAATC
851 CCGATATTGC CACTATATG GGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGTGTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMSAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYX GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTCYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

	10	20	30	40	50	60
m582.pep	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPSSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPSSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
	250	260	270	280	290	300
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

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```

m582.pep  LNDRQNVYSLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          |||
g582       LNDRQNVYSLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          |||
g582       GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCTGCG CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACCAATTCCG
401 CCAACTATGC CCCGGGTTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGACAGC AGAAACGTGC GGAACCAAAA TTGAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCAAAAG ATCCGATTGG CAGATTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCCA ATACGGATTA CAAACCTGAA ATTTTCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTTCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACGCG
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTCCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPIRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDRQNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          |||
a582       MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          |||
a582       LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

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m582.pep	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
a582	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
	130 140 150 160 170 180
m582.pep	190 200 210 220 230 240
a582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
	190 200 210 220 230 240
m582.pep	250 260 270 280 290 300
a582	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYMGYGDVVKLQYR
	250 260 270 280 290 300
m582.pep	310 320 330 340 350 360
a582	LNDQRNVSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
	310 320 330 340 350 360
m582.pep	370
a582	GLMFNDLDGIX
	370

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatattacc catcttgccct tctgtgcctt
51  ttgctgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgcgac tgtaaccgat gccacagcgt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacgca ctcaacgcat cgctcatcgc cgcgcccggg ttgtcggcgg
351 ttacgccggg tactgcgacc aacccgacgg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRDLP VGYGQCQNQG AQYCGNGEGY RFETQPHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCCGAA AGAGCGAGAC TGTAAACGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAAGCGA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACAGGGC GCACAATACT GCGGCAATGS CGAGGGGTAT CGGTTTGAAA

```

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551 CCCAATTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG  
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ  
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI  
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG  
151 QQRPSLRDLP VGYGQCQNG AQCNGEGY RFETQFHHID LRKKDRPEKS  
201 EK\*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAA	GIGRNGSQQ	QFGKSETVTD
g583	MIIDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAA	GIGRNGSQQ	QFGKSETVTD
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDK	QISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTQRIHR	RARFVGGYAG
g583	AQRFSKNGDK	QISDTHPQP	CFEQTARNHN	CDGNQPNQRI	GERTQRIHR	RARFVGGYAG
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRDLP	VGYGQCQNGA	AQCNGEGY
g583	YCDQPDGNNR	QRAQRHGLAD	NGGNHTDKHG	QQRPSLRDLP	VGYGQCQNGA	AQCNGEGY
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHHID	LRKKDRPEKSEKX				
g583	RFETQFHHID	LRKKDRPEKSEKX				
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCTT TCTGTGCTTT  
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT  
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG  
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA  
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC  
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT  
301 GGGCAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCCGCGG  
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC  
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC  
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA  
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA  
551 CCCAATTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG  
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAA GIGRNGSQQ  
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI  
101 GERTQRIHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG  
151 QQRPSLRDLP VGYGQCQNG AQCNGEGY RFETQFHHID LRKKDRPEKS  
201 EK\*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT	HLAFCAFCGI	GAVTAGNRLH	NRMYNAAAAA	GIGRNGSQQ	QFGKSETVTD

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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD
              10      20      30      40      50      60

              70      80      90      100     110     120
m583.pep  AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNPNQRIGERTQRIAHRRARFVGGYAG
            |||||
a583      AQRFSKNGDKQISDTHPQPCFEQTARNHNCNQNPNQRIGERTQRIAHRRTRFVGGYAG
              70      80      90      100     110     120

              130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
            |||||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
              130     140     150     160     170     180

              190     200
m583.pep  RFETQFHHIDLRKKDRPEKSEKX
            |||||
a583      RFETQFHHIDLRKKDRPEKSEKX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

```

g584.seq..
1  atgctgcgtt ctattttggc ggcttcctcg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatatgtg cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcgcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttgta aaaaattcaa
201 caatttcacc agaaaatcga aaaatgtag ctttaaaacc gaattggtat
251 cgcgcagtcg gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag ggcgaggcca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgcggtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcggttctg ggtgcgtccc gttataaaat cgtcaaatg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtta cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

```

g584.pep Length..
1  MLRSILAASL LAVSFPAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNAVNA EFVKKFNNFT RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGA VRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

```

m584.seq..
1  ATGTTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAATCGA AAAATGTTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTAAAG GTCGAAGGTA GAGATTTGA
351 TGAGTTAAAC CGTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCKATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTT GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

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m584.pep..

```

1  MLRLVLAASL SAVSFPAABE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASL	SAVSFPAAAE	ALNYNIVEFS	ESAGVEVAQD	TMSARFQVTA	EGRDKNVNA
	:					
g584	MLRSILAASL	LAVSFPAABE	ALNYNIVEFS	ESAGIEVAQD	TMSARFQVAAE	EGRDKNVNA
	10	20	30	40	50	60
	70	80	90	100	110	120
m584.pep	EFVKKFNKFI	RIRKSKNGSF	KTELVSRSAM	PRYQYTNRR	RIQTGWEE	RAEFKVEGR
g584	EFVKKFNFT	RIRKSKNGSF	KTELVSRSAM	PRYQYTNRR	RIQTGWEE	RAEFKAEGR
	70	80	90	100	110	120
	130	140	150	160	170	180
m584.pep	RFIADIQADA	ALXYTDFHVS	RERRNEVIXQ	VSKDAVLRFK	KARAEKLAV	LGLASGYKIV
g584	RFIADVQD	ASLEDTDFS	VSRERRNEV	IDQVSKDAV	LRFKARAEK	LAVLGLASGY
	130	140	150	160	170	180
	190	200	210	220	230	
m584.pep	NLGHIGSHIA	GGGAAQAKML	RAMPMAASVN	MEGADSAAPG	VEEISISVNG	TVQF*
	:					
g584	NFGQIGSHIA	GDGAVRAKML	RAMPMAASVN	MMKGTDSAPG	VEEISISVNG	TVQF*
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTGGGC GGCTTCCCTG CTG.....
51  ..... ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACCC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGCCTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTTT CCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTT GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATCCGCG
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCACT
701 TCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1802; ORF 584.a&gt;:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDAVN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASL	SAVSFPAAAE	ALNYNIVEFS	ESAGVEVAQD	TMSARFQVTA	EGRDKNVNA
	:					
a584	MLRSILAASL	-----	IVEFS	ESAGVEAVQD	TMSARFQVTA	EGRDKNVNA
	10	20	30	40		



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	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPQYQYTNRRITQGWEEAEFKVEGRDFDELN					
a584	EFVKKFNKFIRKSKNGSFKTELVSRSAMPQYQYTNRRITQGWEEAEFKVEGRDFDELN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt tccaacgcat tttcgccaca ttttgcgcgg ttatcgctctg
51  cgcaatcttt gtggcgagtt tttctttttg gctgggtgcag aacacccttg
101 cggaaaacca attcaaccaa cgccgcacca tcgaaaccac attgatgggc
151 agcattattt cgcatttcaa gacacggggc gacaacggcg cgcgcgaaat
201 cctgaccgaa tggaaaaaca gccccgtctc atccgcggtt tacgtcatac
251 agggcgacga gaaaaaagac atcttaaac gctatatcga caattacacc
301 atagaacgcg cccggtgtgt tgccgccaac aaccccgatt ccaaccttgt
351 cgcgacgaa tacgaccgtt tcggcggaaga atacctgttc ttcatataag
401 gctgggacaa ccaccaggca caacgcctgc ccagcccgct gtttatcccg
451 ggcctgccgc ttgccccgat ttggcagcaa ttcatcatcc tctccttcac
501 catcattgtc ggactgctga tggcatatat ccttgccggc aacattgcca
551 aacccatcag aatcttaggc aacggcatgg acaggggtgc agaacgagaa
601 cttgaagacc gcgtttgcca acaggttcgc gaccgcgacg acgaattggc
651 cgatgttgc atgcaattcg acacaatggt ggaaaaactg gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51  SIISAFKTRG DNGAREILTE WKNSPVSSAV YVIQGEKKD ILNRYIDNYT
101 IERARLFAAN NPHSNLVRIE YDRFGEEYLF FIKGWDNHQA QRLPSPLFIP
151 GLPLAPIWHE FIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVAERE
201 LEDRVCCQVR DRDELADVA MQFDTMVEKL E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT TCCAACGCAT TTTGCCACA TTTTGC CGG TTATCGTCTG
51  TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCG GGCACGCGG GACGCGGGTG CGCGCGAAAT
201 CCGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAAGAT ATCCTGAACC GGTATATCGA CAGCTATACC
301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTC TTCAACAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCTGC CCAGCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCAGCAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGACTGCTGA TGGCATATAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AACCGAGAA
601 CTTGAAACCC GTATCTCCA ACAGGTCGAC GACGCGACG ACGAATTGTC
651 CCATCTTGCC ATCCAATTCG ACAAATGGT GAAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCAG TCTCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAAGT ACCCGCATGG
851 ATACGCTGCG CGGGGAACTG TTAACCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AACCGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAAACA CAACCATCT TGCCAACGAA

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA  
 1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC  
 1151 ACTGGATAAT CGACGTTACC GACAAACGGCC CCGGCGTGA CGAAATGCAG  
 1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA  
 1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC  
 1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG  
 1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC  
 1401 GAACTGA

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG  
 51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDK ILNRYIDSYT  
 101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI  
 151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE  
 201 LETRISQQVD DRDDELHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS  
 251 PLARMQAIVG LIQAQPKQKE QYLKRLEGEL TRMDTLAGEL LTLRSLTSN  
 301 MALEKESLKL LPFLGNLVED NQSIQKNGQ TVTSLADGKI PENTTILANE  
 351 SYLYRAFQNV IRNAVNSPE GSTILINIGQ DHKHWIDVT DNGPGVDEMQ  
 401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM  
 451 RFLPKKKTG SKTEKSAN\*

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
g585	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFKTRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEKDKILNRYIDSYTIERARLFAAGHPHNSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQGDEKDKILNRYIDNYTIERARLFAANNPHNSNLVRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPPLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
g585	YDRFGEEYLFPIKQWGNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNGMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL					
g585	NIAKPIRILGNGMDRVAERELEDRCQVDRDRDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGELTLRSLTSN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

1 ATGAAACTGT TCCAACGCAT CTTGCCACA TTTTGC GCGG TTATCGTCTG  
 51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG  
 101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC  
 151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGT CGCGCGAAAT  
 201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC  
 251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC  
 301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT  
 351 CCATATCGAA TACGACCGCT TCGCGGAAGA ATACCTGTTC TTCACCAAAG  
 401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC  
 451 GGCCTGCCGC TCGCCCGGAT TTGGCACGAA CTCATCATAT TGTCTTCAT  
 501 CATCATCGTC GGACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA  
 551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA  
 601 CTTGAAACCC GTATCTCCCA ACAGGTGCAC GACCGCGACG ACGAATTGTC

```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GAAAAAATC GAAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTC
751 CCCCTTGCGC GCATGCAGGC AATTGTGCGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAAGT TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGG CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```

1 MKLFQIRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDDEKDD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQKE QYLKRLEGEL TRMDTLAGE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNYSP EGSTILINIG DHKHWIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
a585	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG					
	10	20	30	40	50	60
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDDEKDDILNRYIDSYTIERARLFAAGHPHNSLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQGDDEKDDILHRYIDSYTIERARLFAAGHPHNSLVHIE					
	70	80	90	100	110	120
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPLLIPLPLAPIWHELIILSFIIIVGLLMAYILAG					
a585	YDRFGEEYLF FTKDWDKLQARRLPSPLLIPLPLAPIWHELIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
m585.pep	NIAKPIRILGNMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL					
a585	NIAKPIRILGNMDRVANGELETRISQQVDDRDELHLAIQFDKMVEKLEKLVAKERHL					
	190	200	210	220	230	240
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPKQEQYLKRLEGELTRMDTLAGE LTLRLETSN					
a585	LHHVSHEMRSPLARMQAIVGLIQAQPKQEQYLKRLEGELTRMDTLAGE LTLRLETSN					
	250	260	270	280	290	300
m585.pep	MALEKESLKLPLFLGNLVEDNQSIAQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV					
a585	MALEKESLKLPLFLGNLVEDNQSIAQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV					

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1 atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51 ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tcggtacttt gggatacacg gtttaccaaa accgtgctggc ttcccaaat
151 caggaagcgg cggcggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agcccccga aagcgaatca atgccgaact gtccaaactc caacaagct
251 acccccattc catttcggcc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcggtt cgatgttgcc gaaggtcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgtc
401 tggcggttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctgcacacgc cgggttaggc ggacttcgcc cccctgctga tggaaactaa
501 aggcgatggt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggg tttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1 MAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRASQN
51 QEAAAVLANI VEKAQNKAPQ SEINAELSKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQEKSQEA LKNYGQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1 ATGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAACT TTAATATTT
51 TTGGAAAACC ACGGGCAAAT GGCTGTTGC CTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTAGAAAAAG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAACTC CAACAAGCT
251 ACCCGCATTC CATTTCGCCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTCCAAC CAAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGCGTTGT GTTGTGCAA CAAAAAAAAT ACGATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAAG CCAGGAAGCC TTAAAAAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1 MAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN
51 QEAAAVLANI VEKAQSKAPQ SEINAELTKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHLKWVLSN QKDSLIQALA AQLRGVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAHLEEQQE LDNFKYFWKT TGKWL <del>FALLI</del> LAALGYLGYT VYQNRKVSQN QEAAAVLANI					

914

```

g586      MAAHLEEQQE LDNFKYFWKTTGKWLFA LLILAALGYLG YTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKA PQSEINAELSKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180

           190     200     210
m586.pep  LKNYGQALEKMPQDSVGRELVQMKLDSLKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGRELVQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1  ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAGACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTCCAAC CAAAAGACA GCCTGATCCA GGCCTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTTCGAA CAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGAATTCGCC CCCCTGCTGA TGGAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAATAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTG GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1  MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLG YTVYQNRAASQN
51  QEAAAVLANI VEKAQNKA PQSEINAELAKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLWVLSN QKDSLIALAA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

m586/a586  97.6% identity in 209 aa overlap

           10      20      30      40      50      60
m586.pep  MAAHLEEQQE LDNFKYFWKTTGKWLFA LLILAALGYLG YTVYQNRAASQNQEAAAVLANI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQE LDNFKYFWKTTGKWLFAVLI LAALGYLG YTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKA PQSEINAELAKLQQSYPHSISAAQATLMAAAEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180

```

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVMKLDLKLX
                |||||
a586          LKNYGQALEKMPQDSVGRELVMKLDLKLX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaaaactc acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSNR
51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCAGT TTACATTCOA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGAATAC CGACATTTC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGCT
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

916

```

m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENSRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           TGATSFIPTEIQENGSDMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

                130     140     150     160     170     180
m587.pep      NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKRRGLCPFYNLRYNEY
                130     140     150     160     170     180

                190     200     210     220     230     240
m587.pep      LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1  ATGAAGCGCA TCTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCAGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAGGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGTGCCCTA CCGTATCAAC GGCAGCAAAA CCCTTCAAG CAACACCAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS ITYLNSENN
51 AELAAPVYIQ TGATSFIPTE IQENGSDML VGTGLGLR YGLTGNTDI
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

                10      20      30      40      50      60
m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a587           TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

```

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	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

g588.seq

```

1   atgcttaaac atctcgcatc cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacy gcaaattcga
201 cgggcaaggc gtttataacc ttgccgccgg ccgcgaagta tttctcgagc
251 cggttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaaacaaag gcttggcaca cggcagggtc gccgcctcgc aaaacggcga
351 aacctctttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

g588.pep..

```

1   MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRNYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

m588.seq..

```

1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCCTGA CTTCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAAACCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGTTTCG TTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

m588.pep..

```

1   MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENMIK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10            20            30            40            50            60



918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGKPSGKGIWRCRDRGRYTGTS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGQVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSNQGETLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g588        FKNGKFDGQGQVYTVAAAGREVFLEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMIKEVKLPKNKX
g588        YYEMRTRHDX
             130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51 CGCCGCGTCC GCCGTTCTGA CTCCTATCA AGAACCCGGC TGCACCTACG
101 AAGCGGATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPKAGKGTWR
51 CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSNQGETLF IMKCENGMIK EVKLPKNK*

m588/a588    96.4% identity in 138 aa overlap

             10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGQVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSNQGETLF
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a588        FKNGKFDGQGQVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSNQGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMIKEVKLPKNKX
             |||||:|||||:|||||:|||||:|||||:|||||:|||||
a588        IMKCENGMIKEVKLPKNKX
             130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51 tgcttcgcgc attgaaaaag tgttgaacaa aaaagatttt gtcgaatcgg
101 cgggagtga ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcggaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggctg gcggttgtgg cttttgctga ccatcaatat cccgttcctt

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919

```

301 atcgggtatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgcac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggctgta tgggtatcgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcacaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgcgcaccca agtcaactcg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttacc
751 cgaccaaac acggcgaacg catcgtctgc gacggcatta tcgaaagcgg
801 cagcgtttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggc gggcggcaaa gtgttggcgg gcgcgtgât gaccgaaggc
901 acgtgtgtgt accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgtctctcg aagcacaagg cagttaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaaactg ctggggcatc
1051 gcgctcttga cttttatcgt tgcttggctg attaaggcg attgacggg
1101 cgcactgatg cagcgcgttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggtctggc gacccctgcc gcgattatgg tcggcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgcgctttat tacgttcccg acagcggctt tgacgaagac
1351 gcttctgacc gcatcgccgc cgcgctcgag caaaacgcgc cccaccgct
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggttg gagattcccg
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagt
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgc atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 acaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccg tggcgatggg
1851 cggcgacggc atcaacgacg cgcgcgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgcg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacggtt gaaaacatca agcaaaacct atttttcgcc ttctctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcgggt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADI AKI IEKTYGGAKE KTEDTL PQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMLKG LNWRH DMI PPVWQFVLAS IVQLWLAI PF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHYFE AGVMVIGFVS
201 LGKFLEHRTK KSSINSLG LL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTV ALM HAVAVLVIA C PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKS GK AEFAELTL PK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAI GR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAG TGTGAAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTTT

```

920

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATTG AGGCGGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACTGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTT GCGGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GCGGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TCGCGCGTA GCCGATAAAG
1001 CCGCTGCGGT ATTCTGTCCT GCCGTCTGG GCATTGCGTT GTTGAATTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CTTGCGCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCTGG ATGGGCAAG CGGTAAACA CGGTATTGTTG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCGC
1301 TTTATTGCGT TCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCGCGCG TCGAACAAAA CGCCGCCCAT CCGCTCGCC GTGCCATCGT
1401 CTCCGCGGCC CAAGCGCGCG GTTGGACAT TCCGCGCGCA CAAAACGCAC
1451 AAACCGTTGT CCGCGCAGGC ATTACCGCGG AAGTGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGCTCTCA GTCGATAACA
1601 AACCATCGG CGCATTGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCCT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AACTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCG
1951 TCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTG
2051 CTCTCGCCGC GCTTGGCTTT TTAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

```

m589.pep..
1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDD
51  KTSVADIARI IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLFTINVFFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVVLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVIYFEVGMV IGFVSLGKFL
201 EHRTKKSSLN SLGLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251 ERIAADGIEI SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSSVYR
301 ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTF
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEEA AHVDAVVLK TGTLTGESPQ VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIARI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

921

g589           MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIKI  
                  10           20           30           40           50           60

                  70           80           90           100           1           110  
m589.pep       IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVFPFLIGMAGMMIG-----RHDWMI  
                  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
g589           IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWTRHDWMI  
                  70           80           90           100           110           120

                  120           130           140           150           160           170  
m589.pep       PPLWQFALASVVQLWLAIIFYKSASWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA  
                  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
g589           PPVWQFVLASIVQLWLAIIFYKSASWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA  
                  130           140           150           160           170           180

                  180           190           200           210           220           230  
m589.pep       AYGMAHVYFEVGMVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP  
                  |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
g589           AHGMAHVYFEAGVMVIGFVSLGKFEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP  
                  190           200           210           220           230           240

                  240           250           260           270           280           290  
m589.pep       IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG  
                  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
g589           IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG  
                  250           260           270           280           290           300

                  300           310           320           330           340           350  
m589.pep       SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL  
                  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
g589           SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVVGIALLTFFIVAWL  
                  310           320           330           340           350           360

922

	360	370	380	390	400	410
m589.pep	IKGDWTVVALMHAVAVLVIAICPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVVALMHAVAVLVIAICPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDALYRIAAVEQNAAHPLARAIIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDALYRIAAVEQNAAHPLARAIIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEEVEGVGLVKSAGKAEFAELALPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIIGRLKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIIGRLKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINAPALAAANVSFAMKGGADVAHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINAPALAAANVSFAMKGGADVAHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPFVIAGAAMAASSSVSLNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPFVIAGAAMAASSSVSLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589.seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAG TGTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCTTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGACA CCGCACCAAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAACTCA CGCAAACCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGCTACCC ATCGACCAAG TGCAAATCGG CGACCTAATC
751 CGCGCCAATC ACGGCGAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG CCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCCGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCTG TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATATCG TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

```

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCAGGC GCGCGGTTG GAGATTCCTCA
1451 CCGCACAAA TGCCCAACC ATGTGCGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAA GCCGAATTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAG CGGCAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CGCCGAAGC CATAGGCGGT CTGAAAAAAC ACAATATCGA
1701 TGCTATATT ATGAGCGGCG ATAACCAAGG CACGCTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCCGCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTGCGC AACACACCGC ATCGGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```

a589.pep
1  MQQKVRFOIE GMTQACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIARI IEKTGYGAKE KTEDTLPPQE AEHHIGWRLW LLLAINIPEL
101 IGMVGMMLKG LNWTRHDWML SPLQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKPVAAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

m589/a589 94.9% identity in 725 aa overlap

      10      20      30      40      50      60
m589.pep MQQKIRFQIEGMTQACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSDKTSVADIARI
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      MQQKVRFOIEGMTQACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSDKTSVADIARI
      10      20      30      40      50      60

      70      80      90      100     110
m589.pep IEKTGYGAKEKTEDTLPPQEAHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      IEKTGYGAKEKTEDTLPPQEAHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
      70      80      90      100     110     120

      120     130     140     150     160     170
m589.pep PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
      || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      SPLQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
      130     140     150     160     170     180

      180     190     200     210     220     230
m589.pep AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
      190     200     210     220     230     240

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m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
a589	IDQVQIGDLIRANHGERIAADGII	ESGSGWADESHLTGESNPEEK	KAGGKVL	LAGALMTEG		
	250	260	270	280	290	300
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VPVAVGIAL	LTFFIVTWL		
a589	SVVYRAAQLGSQTLGDMMNAL	SEAQGSKAPIARVADKAAAVF	VPVAVGIAL	LTFFIATWL		
	310	320	330	340	350	360
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAAHVDA			
a589	IKGDWTLALMHAVAVLVIA	CPALGLATPAAIMVGMGKAV	KHGIWFKDAAAMEEAAHVDA			
	370	380	390	400	410	420
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGSPQVA	AVYCVPD	SGFDE	DALYRIA	AAVEQNA	AHPLARAI
a589	VVLDKTGTLTGSPQVA	AVYCVPD	SGFDE	DALYRIA	AAVEQNA	AHPLARAI
	430	440	450	460	470	480
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTIVGAGITA	EVGVGLVKAGKAEFAEL	LPKFLDGVWD	IASIVAVS	VDNKP	
a589	EIPTAQNATIVGAGITA	EVGVGLVKAGKAEFAEL	LPKFLDGVWD	IASIVAVS	VNGKP	
	490	500	510	520	530	540
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAE	AIGRLKKNHNDVYIMSGDN	QGTVEYVAK	QLGIAHAF	GNMSPRDK	
a589	IGAFALADALKADTAE	AIGRLKKNHNDVYIMSGDN	QGTVEYVAK	QLGIAHAF	GNMSPRDK	
	550	560	570	580	590	600
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAM	VGDI	NDAPALAAANVS	FAMKGGAD	VAEHTASAT	LMQHSVNQLA
a589	AAEVQKLKAAGKTVAM	VGDI	NDAPALAAANVS	FAMKGGAD	VAEHTASAT	LMQHSVNQLA
	610	620	630	640	650	660
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNL	FFAFFYNILGIPLAAL	GFLNPVI	AGAMAASSV	SVLSNALRLK	
a589	DALLVSQATLKNIKQNL	FFAFFYNILGIPLAAL	GFLNPVI	AGAMAASSV	SVLSNALRLK	
	670	680	690	700	710	720
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:  
g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccagc
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtaa accatatcac gcacggccct
301 ttcgcccggc gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaag ttttggaacg ctttttggg aaacaagttc
401 cgggttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca

```

```

501 ctgggaaggc ctgacggggg aaacgggtta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccg cgtttgaaaa agcgcatctt gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcgcg gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaaggcg gttccgtttc
901 gatacgttgg tgcacggcga tgaataaac ggcccgctgg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcgaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcccaaaaa atgttgaag atttggcggg aagtcaggct ggaaatattt
1301 tcagtgttaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgct gatggtggac agtacggctc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg ggaacgct gcaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttcggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAES LTQQQKILQK TGFLTIVESHQ
51 YDRGWFSTSE TTVIRLKPEL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLRFPG KQVPVSLANT VYFNGSGKME
151 VSVPAFYDYE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLT EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA PSTKTGESGA FIDSEGRFRF
301 DTLVYGDYKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMMKEDLN
401 QLGLMLKTE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIAE
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNVAL KLNKTLQNE
501 PDPDFDEGDM VSGQPH*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGGTTTACCT CTATGGAAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGGCGTACAT TGAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAATAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG. CTGCACT GGGAAGCCT
351 GACGGAGAAA ACGGTTTATC AAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTGTGTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCCGG
451 TTTGAAAAG TGCAATTCGA TCGGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAAGTGGT CAATCTTGT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTCAAC AACAATCCCG TATTGGACAT
951 TAAACTTTC CGATTACGC TGCCATCGGG AAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTT AGCGTCAATG
1151 CCGAAGATGA GCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATC TGCCATTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:



926

## m590.pep..(partial)

```

1  ..WFTSMETTVI RLKPELNNNA RYKLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE FKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSVP
101 AFDYEELSGI XLHWEKLTGE TVYQKGFSY RNGYDAPLFK IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT EQRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMFKDM KKEDLNQLGL
351 MLKKTEADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT NGDQIDTAIS LKNNQLKLNG KTLQNEPEPD
451 FDEGGMVSEP QQ*

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m590 / g590 93.1% identity in 462 aa overlap

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                                10      20      30
m590.pep                      WFTSMETTVIRLKPPELLNNARKYLPDNLKT
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      VKAESLTQQQKILQKTGFLTVESHQYDRGWFTSTETTIVIRLKPPELLHNAQKYLDPNLKI
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m590.pep      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      VLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m590.pep      GSGKMEVSVPAFDYEELSGIXLHWEKLTGETVYQKGFSYRNGYDAPLFKIKLADKGDAA
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFSYRNSYDAPLFKIKLADKGDAA
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m590.pep      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m590.pep      PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGGQFRFDTLVYGEDEKYGPLDIHIAAEHLDA
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGEDEKYGPLDIHIAAEHLDA
                                270     280     290     300     310     320

                                280     290     300     310     320     330
m590.pep      SALTVLKRKFQAISAKKMTTEEQRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      SALTVLKRKFQAISAKKMTTEEQRNDLIAAVKGDASGLFTHDPVLNLIKIFRFTLPQKID
                                330     340     350     360     370     380

                                340     350     360     370     380     390
m590.pep      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      VGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEA
                                390     400     410     420     430     440

                                400     410     420     430     440     450
m590.pep      RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQLKLNGKTLQNEPEPD
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      RASLADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNALKLNGKTLQNEPDPP
                                450     460     470     480     490     500

                                460
m590.pep      FDEGGMVS-EPQQX
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g590      FDEGDMVSGQPHX
                                510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCCA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCTT
301 TTTGCCGGCG GATTGCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACCG CTATGATGCC CCCTTGTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTC GATTGCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGT
751 GTCATCTTG TTACCGATT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCCTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAATACTT TCCGATTCAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTAAAGACA TGAAGAAGGA AGATTGAAAC
1201 CAATTGGGTT TGATGCTGAA GAAACCGGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE AGFLTVESHQ
51  YERGWFSTTE TTVIRLKEPE LHNAQKYLDP NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLT EKFSLEWKEG VDVNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDKEY GPLDIHIAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTNLGDQID TAISLKNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*

m590/a590 97.8% identity in 462 aa overlap

m590.pep
10 20 30
WFTSMETTVIRLKEPELLNARKYLPDNLKT
|||||

a590
30 40 50 60 70 80
VKAESLTQQQKILQEAGFLTVESHQYERGWFSTETTVIRLKEPELLHNAQKYLDPNLKT

m590.pep
40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||

a590
90 100 110 120 130 140
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN

m590.pep
100 110 120 130 140 150
GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFIKIKLADKGDAA
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928

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|||||
a590  GSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
      150      160      170      180      190      200

      160      170      180      190      200      210
m590.pep FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
      |||||
a590  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKNELVNLVTDLQIGAFIN
      210      220      230      240      250      260

      220      230      240      250      260      270
m590.pep PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
      |||||
a590  PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
      270      280      290      300      310      320

      280      290      300      310      320      330
m590.pep SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSPGKID
      |||||
a590  SALTVLKRKFARISAKKMTEEQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPSPGKID
      330      340      350      360      370      380

      340      350      360      370      380      390
m590.pep VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
      |||||
a590  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
      390      400      410      420      430      440

      400      410      420      430      440      450
m590.pep RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKCTLQNEPEPD
      |||||
a590  RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQLKLNKCTLQNEPEPD
      450      460      470      480      490      500

      460
m590.pep FDEGGMVSEPQQX
      |||||
a590  FDEGGMVSEPQQX
      510

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGGCG GATTCCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTGGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAAATGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCATGCCCG CGTTTGAAAA AGTGCAATTC GATTCCGAAA CTTCAGACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGCT
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGA AAAATAC GGGCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACATCC
1101 CGTATTGGAC ATTA AAACCT TCCGATTCAC GCTGCCATCG GGA AAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGGAAT
1201 CAATTGGGAT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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929

1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT  
 1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC  
 1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC  
 1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT  
 1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA  
 1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA  
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE TGFLTVESHQ  
 51 YERGWFSTME TTIVRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP  
 101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME  
 151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK  
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKNLNE  
 251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF  
 301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFAQISAK KMTEEQIRND  
 351 LIAAVKGEAS GLFTNNPVL DIKTFRFTLP SKIDVGGKIM FKDMKKEDLN  
 401 QLGLMLKKE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD  
 451 INETLRMLVD STVQSMAREK YLTNGDQID TAISLKNQL KLNKLTQNE  
 501 PEPDFDEGGM VSEPPQ\*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAA	ALLGVALGTP	YYLGVKAES	LTQQQKILQE	TGFLTVESHQ	YERGWFSTME
g590	MKKPLISVAA	AVLLGVALGTP	YYLGVKAES	LTQQQKILQKT	TGFLTVESHQ	YDRGWFTSTE
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTIVRLKPEL	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
g590	TTIVRLKPEL	LHNAQKYL	PDNLKIVLEQ	PVTLVNHITHGP	FAGGFGTQAH	IETEFKYAPE
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
g590	TEKVLERFFG	KQVPVSLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDA	PLFKIKLADK	GDAAFEKVHF	DSETSDGINP	LALGSSNLTLE	KFSLEWKEG
g590	FKSYRNSYDA	PLFKIKLADK	GDAAFEKAHFD	SETSDGINP	LALGSSNLTLE	KFSLEWKEG
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKNLNE	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FINSEGQFRF
g590	VDYNVKNLNE	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FIDSEGRFRF
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KKKFAQISAK	KMTEEQIRND	LIAAVKGEAS
g590	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KKKFAQISAK	KMTEEQIRND	LIAAVKGDAS
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVL	DIKTFRFTLP	SGKIDVGGKIM	FKDMKKEDLN	QLGLMLKKE	TEADIRMSIPQK
g590	GLFTHDPVL	NIKIFRFTLP	QCKIDVGGKIM	FKGMKKEDLN	QLGLMLKKE	TEANIRMSIPQK
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRMLVD	STVQSMAREK	YLTNGDQID
g590	MLEDLAVSQA	GNIFSVNAED	EAEARASIA	INETLRMLVD	STVQSMAREK	YLTLDGNQID
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQL	KLNGKTLQNE	PEP	DFDEGGMVS	-EPQQX	

930

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      |:||||| |||||:||||| ||| |:|
g590  TVISLKNNAKLNKLTQNEPDPDFDEGDMVSGQPHX
      490      500      510

a590/m590-1  98.3% identity in 516 aa overlap

      10      20      30      40      50      60
a590.pep  MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQEAGELTVESHQYERGWFTSTE
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYERGWFTSME
      10      20      30      40      50      60

      70      80      90      100     110     120
a590.pep  TTVIRLKPPELLHNAQKYLDPNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    TTVIRLKPPELLNNAQKYLDPNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
      70      80      90      100     110     120

      130     140     150     160     170     180
a590.pep  TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
      130     140     150     160     170     180

      190     200     210     220     230     240
a590.pep  FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETS DGINPLALGSSNLTLEKFSLEWKEG
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETS DGINPLALGSSNLTLEKFSLEWKEG
      190     200     210     220     230     240

      250     260     270     280     290     300
a590.pep  VDYNVKNLNLVNLVLDLQIGAFINPNGSIAPSKIEVGKLAFTKTGESGAFIDSEGQFRF
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    VDYNVKNLNLVNLVLDLQIGAFINPNGSIAPSKIEVGKLAFTKTGESGAFINSEGQFRF
      250     260     270     280     290     300

      310     320     330     340     350     360
a590.pep  GTLVYGDEKYGPLDIHIAAEHLDA SALT V LK R K F A R I S A K K M T E E Q I R N D L I A A V K G E A S
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    DTLVYGDEKYGPLDIHIAAEHLDA SALT V LK R K F A Q I S A K K M T E E Q I R N D L I A A V K G E A S
      310     320     330     340     350     360

      370     380     390     400     410     420
a590.pep  GLFTHNPVLDIKTFRFTLP SGK I D V G G K I M F K D M K K E D L N Q L G L M L K K T E A D I R M S I P O K
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    GLFTNNPVLDIKTFRFTLP SGK I D V G G K I M F K D M K K E D L N Q L G L M L K K T E A D I R M S I P O K
      370     380     390     400     410     420

      430     440     450     460     470     480
a590.pep  MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLR L M V D S T V Q S M A R E K Y L T L N G D Q I D
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLR L M V D S T V Q S M A R E K Y L T L N G D Q I D
      430     440     450     460     470     480

      490     500     510
a590.pep  TAISLKNNAKLNKLTQNEPDPDFDEGDMVSGQPHX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m590-1    TAISLKNNAKLNKLTQNEPDPDFDEGDMVSGQPHX
      490     500     510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```

g591.seq
1  TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TCGGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCGCCC AAGCGCATCG CCATCGTCGC CGCCGGTCCG
301 CTGACCAACC TCGCActggc ggTTTGTCTG TACGGACTGa gctTtctctt
351 cggcgtaaCC GAACTGCGGC Cctatgtcgg cacagtcaA cccgacaccg

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931

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTATCGc ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCgggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAacagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGCCCGCCTT CTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

```

g591.pep..
1  LQTLAIFIA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRGR
51  DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSFAEKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFGALMM LMMAAFFND VTRLIG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

```

m591.seq
1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCTGATTT TGGTCAGCCT
51  GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CTTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTATCG CTGATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTGCGCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

932

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKR
51 DTEWCLAPIP LGGYVKMVD REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNLPVPVLDGGHL
401 VFYTAEWIRG KPLGERVONI GLRFGALMM LMAVAFFEND VTRLLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

m591.pep	10	20	30	40	50	60
	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKR	GDTEWCLAPIP
g591	10	20	30	40	50	60
	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKR	GDTEWCLAPIP
m591.pep	70	80	90	100	110	120
	LGGYVKMVD	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
g591	70	80	90	100	110	120
	LGGYVKMVD	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
m591.pep	130	140	150	160	170	180
	ELRPYVGTVE	PDTIARAGF	QSGDKIQSVN	GTPVADWGS	AQTEIVLNLE	AGKVAVGVQTA
g591	130	140	150	160	170	180
	ELRPYVGTVE	PDTVAARTG	FQSGDKIQSV	GVSVQDWSSA	QTEIVLNLE	AGKVAVGVQTA
m591.pep	190	200	210	220	230	240
	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
g591	190	200	210	220	230	240
	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITTVAGG	VEKGSPEAKA	GLKPGDRLTA
m591.pep	250	260	270	280	290	300
	ADGKPIASWQ	EWANLTRQSP	GKKITLNYER	AGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	250	260	270	280	290	300
	ADGKPIASWQ	EWANLTRQSP	GKKITLTYER	AGQHTADIR	PDTVEQPDHT	LIGRVGLRPQ
m591.pep	310	320	330	340	350	360
	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
g591	310	320	330	340	350	360
	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
m591.pep	370	380	390	400	410	420
	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLP	VVPVLDGGHL	VFYTAEWIRG	KPLGERVONI
g591	370	380	390	400	410	420
	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLP	VVPVLDGGHL	VFYTVIEWIRG	KPLGERVONI
m591.pep	430	440				
	GLRFGALMM	LMAVAFFEND	VTRLLGX			
g591	430	440				
	GLRFGALMM	LMAAAFFEND	VTRLLGX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:  
a591.seq

933

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TCGGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCTG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGCGCGC GTGGAAGGAG GCAGCCCCG CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCGCGAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AACTAATCA GCGCAACGC CTCCGTCAGC
1051 CATATTCCG GTCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT GGCACGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCG TTTTGACCG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACCGCT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51  DTEWCLAPIP LGGYVKMVD TREGVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMAVAFFND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

```

          10      20      30      40      50      60
m591.pep  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG DTEWCLAPIP
          |||||
a591      LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG DTEWCLAPIP
          10      20      30      40      50      60

          70      80      90      100     110     120
m591.pep  LGGYVKMVD TREGVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          |||||
a591      LGGYVKMVD TREGVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT
          70      80      90      100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTV E PDTIARAGF QSGDKIQSVNGT P VADWGS AQTEIVLNLEAGKVAVGVQTA
          |||||
a591      ELRPYVGTV E PDTIARAGF QSGDKIQSVNGT P VADWGS AQTEIVLNLEAGKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTID AAGTPEAGKI AKNQGYIGL MPFKITTVAGG VEKGSPEAKAGL KPGDRLTA
          |||||
a591      SGAQTVRTID AAGTPEAGKI AKNQGYIGL MPFKITTVAGG VEKGSPEAKAGL KPGDRLTA
          190     200     210     220     230     240

```



934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQTHADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQTHADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVVISLGVNLNLPVPVLDGGHLVFTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVVISLGVNLNLPVPVLDGGHLVFTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg  acgtgttcgg  tcagattttt  tcgggcgcgt  tcaaattcga
51  cgcggcagca  ggcggcttac  tcggcggtct  gatttcgcaa  acgatgatga
101  tgggcatcaa  acgcggcctg  tattccaacg  aggcgggtat  gggttccgcg
151  ccgaacgccc  ccgcgcgcgc  cgaagtgaag  caccctgttt  cgcaaggtat
201  gattcaaatg  ctgggcgtgt  ttgtcgatac  catcatcggt  tgttcttgca
251  ccgccttcat  catcttgatt  taccaacagc  cttatggcga  tttagcggtt
301  ggcgcgtcga  cgcaggcggc  gattgtcagc  caagtggggc  aatggggcgc
351  gggtttcctc  gccgtcatcc  tgtttatggt  tgccctttcc  accgttatcg
401  gcaactatgc  ctatgccgag  tccaacgtcc  aattcatcaa  aagccattgg
451  ctgattaccg  ccgttttccg  tatgctggtt  ttggcgtggg  tctatttcgg
501  cgcggttgcc  aatgtgcctt  tggctcggga  tatggcggat  atggcgatgg
551  gcatcatggc  gtggatcaac  ctgctcgcca  tcctgctgct  ctgcgcattg
601  gcgtttatgc  tgctgcgcga  ttacaccgcc  aagctgaaaa  tgggcaaaag
651  ccccgagtcc  aaactttccg  aacatccggg  cctgaaacgc  cgcacaaat
701  ccgatgtttg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF  SGAFKFDAAG  GLLGGLISQ  TMMGIKRL  YSNEAGMGA
51  PNAAAAEVK  HPVSQGMQ  LGVFVDII  CSCTAFIIL  YQQPYGDLG
101  AALTQAAIVS  QVGQWAGFL  AVILFMFAPS  TVIGNYAYAE  SNVQFIKSHW
151  LITAVFRMLV  LAWVYFGAVA  NVPLVDMAD  MAMGIMAWIN  LVAILLLSPL
201  AFMLLRDYTA  KLKMGKDFE  KLSEHPGLKR  RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG  ACGTGTTCGG  TCAGATTTT  TCGGGCGCGT  TCAAATTCGA
51  CGCGGCAGCA  GCGGCTTAC  TCGGCGGTCT  GATTTCGCAA  ACGATGATGA
101  TGGGCATCAA  ACGCGGCTG  TATTCCAACG  AGGCGGGTAT  GGGTTCCGCG
151  CCGAACCCGC  CCGCCGCCGC  CGAAGTGAAA  CACCCTGTTT  CGCAAGGTAT
201  GATTCAAAAT  CTGGGCGTGT  TTGTCGATAC  CATCATCGTT  TGTCTTGCA
251  CCGCCTTCAT  CATCTTGATT  TACCAACAGC  CTTACGGCGA  TTTGAGCGGT
301  GCGGCGCTGA  CGCAGGCGGC  GATTGTCAGC  CAAGTGGGGC  AATGGGGCGC
351  GGGCTTCCTC  GCCGTCATCC  TGTATTATGT  TGCCCTTTCC  ACCGTTATCG
401  GCAACTATGC  CTATGCCGAG  TCCAACGTCC  AATTATCAA  AAGCCATTGG
451  CTGATTACCG  CCGTTTTCG  TATGCTGGTT  TTGGCGTGGG  TCTATTTCGG
501  CGCGGTTGCC  AATGTGCCTT  TGGTCTGGGA  TATGGCGGAT  ATGGCGATGG
551  GCATTATGGC  GTGGATCAAC  CTTGTCGCCA  TCCTGCTGCT  CTCGCCCTTG

```

935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCCAGATTG AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..  
 1 MIPDVFGQIF SGAFKFDAAA GLLGLISQ TMMGIKRL YSNEAGMGS  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQQPYGDLG  
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592 / g592 100.0% identity in 237 aa overlap

m592.pep	10	20	30	40	50	60
	MIPDVFGQIFSGAFKFDAAAAGLLGLISQTMGMGIKRLYSNEAGMGSAPNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAAGLLGLISQTMGMGIKRLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
m592.pep	70	80	90	100	110	120
	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWGAGFL					
g592	HPVSQGMQIMLGVFVDIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
m592.pep	130	140	150	160	170	180
	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
m592.pep	190	200	210	220	230	
	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq  
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA  
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTGCAA ACGATGATGA  
 101 TGGGCATCAA ACGCGCCTG TATCCAACG AGGCGGGTAT GGGTCCGCG  
 151 CCGAACGCCG CCGCCGCCG CGAAGTGAAA CACCCTGTT CGCAAGGTAT  
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTTCTTGCA  
 251 CCGCCTTCAT CATCTTGAT TACCAACAGC CTACGGCGA TTTGAGCGGT  
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGCGC  
 351 GGGCTTCCTC GCCGTCATCC TGTATTGTT TGCCTTTCC ACCGTTATCG  
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG  
 451 CTGATTACCG CCGTTTCCG TATGCTGGT TTGGCGTGG TCTATTTCGG  
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG  
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG  
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCCCAGATTG AACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep  
 1 MIPDVFGQIF SGAFKFDAAA GLLGLISQ TMMGIKRL YSNEAGMGS  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQQPYGDLG  
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1   atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatac
151 gtcgggcggg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgccg gaaaaacgcc gtatctcgct gatgttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaagccga agccgaacgc ctgcgcctgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacgggtg gcaactggcg gcgctttggt tgtccgccct
451 tccctgctgt tgctggatga atcgtttcc agtttgaca cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcy gtacgccga
651 aaccttgatt caaacgcctg ccggcgtgca ggtcgcccg ctgatggggc
701 tgccaatac cgacgatgac cgccatattc cgcaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctctg tccctcgcc gcctgccga
801 ctgctccgg cttccgccg tccatccga acacggcga ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtacggtc
901 cgcacccgct tcgatgaagg gcgtatcgct cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1   MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1   ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

```